

## FIG. 1

GAAATTCGGAG GAAATATTCA AATCATAAAC ACATTAALAC ATTTCAGTAG TTGCGGACAC	60
CACACACACAC CACAGCCCGT GGAATATTAC ACTAAALACG ACACTCATTC CAAALAAATCA	120
CCAAACAAAA CATCAATAAA C ATC CAT TCG ATT AAA TGT TTA TTA ACA GCA	171
Met His Trp Ile Lys Cys Leu Leu Thr Ala	
1 5 10	
TTC ATT TCG TTC ACA GTC ATC GTC CAC GTT CAC AGT TCG GCG ACC TTT	219
Phe Ile Cys Phe Thr Val Ile Val Gln Val His Ser Ser Gly Ser Phe	
15 20 25	
CAC TTC CCG CTC AAC TAC TTC ACC AAC CAT CAC CCG CCG CAC AAC CAC	267
Glu Leu Arg Leu Lys Tyr Phe Ser Asn Asp His Gly Arg Asp Asn Glu	
30 35 40	
CGT CCG TCG TCG ACC GCG GAG TCG GAC CGA CCG ACC CCG AAC TCG CTC	315
Gly Arg Cys Cys Ser Gly Glu Ser Asp Gly Ala Thr Gly Lys Cys Leu	
45 50 55	
CGC ACC TCG AAC ACC CCG TTT CCG GTC TCG CTA AAC CAC TAC CAC CCG	363
Gly Ser Cys Lys Thr Arg Phe Arg Val Cys Leu Lys His Tyr Gln Ala	
60 65 70	
AAC ATC CAC ACC ACC TCG CAG TCG ACC TAC CCG CAC GTG ATC ACC CCG	411
Thr Ile Asp Thr Thr Ser Gln Cys Thr Tyr Gly Asp Val Ile Thr Pro	
75 80 85 90	
ATT CTC CCG CAG AAC TCG GTC AAT CTC ACC GAC CCG CAC CCG TTC CAC	459
Ile Leu Gly Glu Asn Ser Val Asn Leu Thr Asp Ala Gln Arg Phe Gln	
95 100 105	
AAC AAC CCG TTC ACC AAT CCC ATC CAG TTC CCC TTC TCG TTC TCA TCG	507
Asn Lys Gly Phe Thr Asn Pro Ile Gln Phe Pro Phe Ser Phe Ser Trp	
110 115 120	
CCG CGT ACC TTC TCG CTC ATC GTC GAG CCG TCG CAT CAT ACC AAC AAT	555
Pro Gly Thr Phe Ser Leu Ile Val Glu Ala Trp His Asp Thr Asn Asn	
125 130 135	
AAC CCG AAT CCG CGA ACC AAC AAC CTC CTC ATC CAG CGA CTC TTC GTC	603
Ser Gly Asn Ala Arg Thr Asn Lys Leu Leu Ile Gln Arg Leu Leu Val	
140 145 150	
CAC CAC GTA CTC CAC GTC TCG TCG GAA TCG AAC ACC AAC AAC TCG GAA	651
Gln Gln Val Leu Glu Val Ser Ser Glu Trp Lys Thr Asn Lys Ser Glu	
155 160 165 170	
TCC CAC TAC ACC TCG CTC GAG TAC CAT TTC CGT GTC ACC TCG CAT CTC	699
Ser Gln Tyr Thr Ser Leu Glu Tyr Asp Phe Arg Val Thr Cys Asp Leu	
175 180 185	
AAC TAC TAC CGA TCG CCG TGT CCC AAC TTC TCG CCG CCC CCG CAC CAT	747
Asn Tyr Tyr Gly Ser Gly Cys Ala Lys Phe Cys Arg Pro Arg Asp Asp	
190 195 200	
TCA TTT CGA CAC TCG ACT TCG TCG GAG ACC CCG GAA ATT ATC TGT TTG	795
Ser Phe Gly His Ser Thr Cys Ser Glu Thr Gly Glu Ile Ile Cys Leu	
205 210 215	
ACC CGA TCG CAC CCG CAT TAC TGT CAC ATA CCC AAA TCG CCG AAA CCG	843
Thr Gly Trp Gln Gly Asp Tyr Cys His Ile Pro Lys Cys Ala Lys Gly	
220 225 230	
TGT GAA CAT CGA CAT TCG GAC AAA CCC AAT CAA TCG GTT TCG CAA CTC	891
Cys Glu His Gly His Cys Asp Lys Pro Asn Gln Cys Val Cys Gln Leu	
235 240 245 250	

## FIG. 1 CONT'D.

CCC TCC AAC GGA GCC TTC TCC AAC GAG TCC GTT CTG GAA CCG AAC TCC Gly Trp Lys Gly Ala Leu Cys Asn Glu Cys Val Leu Glu Pro Asn Cys	939
255 260 265	
ATC CAT GCC ACC TCC AAC AAA CCC TCC ACT TCC ATC TCC AAC GAG GGT Ile His Gly Thr Cys Asn Lys Pro Trp Thr Cys Ile Cys Asn Glu Gly	987
270 275 280	
TCC GGA CCC TTC TAC TCC AAC CAG CAT CTC AAC TAC TCC ACC AAC CAG Trp Gly Gly Leu Tyr Cys Asn Glu Asn Leu Asn Tyr Cys Thr Asn His	1035
285 290 295	
AGA CCC TCC AAC AAT GCC GGA ACC TCC TTC AAC ACC GGC GAG GGA TTC Arg Pro Cys Lys Asn Gly Gly Thr Cys Phe Asn Thr Gly Glu Gly Leu	1083
300 305 310	
TAC ACA TCC AAA TCC GGT CCA GGA TAC ACT GGT CAT CAT TCC GAA AAT Tyr Thr Cys Lys Cys Ala Pro Gly Tyr Ser Gly Asn Asn Cys Glu Asn	1131
315 320 325 330	
GAG ATC TAC TCC TCC GAT CCC CAT CTC AAT CCC TCC CAG AAT GGT GGT Glu Ile Tyr Ser Cys Asn Ala Asn Val Asn Pro Cys Gln Asn Gly Gly	1179
335 340 345	
ACC TCC ATC CAT CAG CCC CAG ACA AAA ACC GGC TAC AAC TGT CAT TCC Thr Cys Ile Asn Glu Pro His Thr Lys Thr Gly Tyr Lys Cys His Cys	1227
350 355 360	
CCC AAC CCC TCC ACC GGA AAC ATC TCC CAG CAG AAA CTC CTC ACC TGT Ala Asn Gly Trp Ser Gly Lys Met Cys Glu Glu Lys Val Leu Thr Cys	1275
365 370 375	
TCC GAG AAA CCC TGT CAT CAG GGA ATC TCC CCC AAC GTT GGT CCT GGC Ser Asn Lys Pro Cys His Gln Gly Ile Cys Arg Asn Val Arg Pro Gly	1323
380 385 390	
TTC GGA AGC AAC GGT CAG GGC TAC CAG TCC GAA TGT CCC ATT GGC TAC Leu Gly Ser Lys Gly Gln Gly Tyr Gln Cys Glu Cys Pro Ile Gly Tyr	1371
395 400 405 410	
AGC GGA CCC AAC TCC GAT CTC CAG CTC GAG AAC TCC AGT CCC AAT CCA Ser Gly Pro Asn Cys Asn Leu Gln Leu Asn Asn Cys Ser Pro Asn Pro	1419
415 420 425	
TCC ATA AAC GGT GGA AGC TGT CAG CCC ACC GGA AAC TGT ATT TCC CCA Cys Ile Asn Gly Gly Ser Cys Gln Pro Ser Gly Lys Cys Ile Cys Pro	1467
430 435 440	
CCC GGA TTT TCC GGA ACC AGA TCC GAG ACC AAC ATT GAG CAT TGT CTT Ala Gly Phe Ser Gly Thr Arg Cys Glu Thr Asn Ile Asn Asn Cys Leu	1515
445 450 455	
CCC CAG CAG TCC CAG AAC GGA GCC ACC TCC ATA CAT ATC GTC AAC CAA Gly His Gln Cys Glu Asn Gly Gly Thr Cys Ile Asn Met Val Asn Gln	1563
460 465 470	
TAT CCC TCC CAA TCC GTT CCC GGT TTC CAT GGC ACC CAG TGT AGT ACC Tyr Arg Cys Gln Cys Val Pro Gly Phe His Gly Thr His Cys Ser Ser	1611
475 480 485 490	
AAA GTT GAG TTC TCC CTC ATC AGA CCG TGT GCC AAT GGA GGA ACC TCC Lys Val Asn Leu Cys Leu Ile Arg Pro Cys Ala Asn Gly Gly Thr Cys	1659
495 500 505	
TTC AAT CTC AAC AAC CAT TAC CAG TCC ACC TGT GGT GGC GGA TTT ACT Leu Asn Leu Asn Asn Asn Tyr Gln Cys Thr Cys Arg Ala Gly Phe Thr	1707
510 515 520	

## FIG. 1 CONT'D.

GGC AAC GAT TCC TCT GTG GAC ATC GAT GAG TCC ACC AGT GGA CCC TGT	1755
Gly Lys Asp Cys Ser Val Asp Ile Asp Glu Cys Ser Ser Gly Pro Cys	
525 530 535	
CAT AAC GGC GGC ACT TCC ATG AAC CCG CTC AAT TCC TTC GAA TCC GTG	1803
His Asp Gly Gly Thr Cys Met Asp Arg Val Asp Ser Phe Glu Cys Val	
540 545 550	
TGT CCC AAT GGT TTC ACC GGC AAC CAG TCC GAT CAG CAG TCC TAC GAT	1851
Cys Ala Asp Gly Thr Arg Gly Lys Glu Cys Asp Glu Glu Ser Tyr Asp	
555 560 565 570	
TCC GTG ACC TTC GAT CCG CAC GAA TAT GGA CCG ACC ACA GAA GCG ACA	1899
Ser Val Thr Phe Asp Ala His Glu Tyr Gly Ala Thr Thr Glu Ala Arg	
575 580 585	
CCC GAT GGT TTG ACC AAT CCG CAG GTA CTC CTA ATT CCT GTT TTC TCC	1947
Ala Asp Gly Leu Thr Asp Ala Glu Val Val Leu Ile Ala Val Phe Ser	
590 595 600	
GTT CCG ATG CCT TTG GTG CCG GTT ATT CCG CCG TCC CTC CTC TTC TCC	1995
Val Ala Met Pro Leu Val Ala Val Ile Ala Ala Cys Val Val Phe Cys	
605 610 615	
ATG AAC CCG AAC CGT AAC CGT GCT CAG GAA AAC CAC GAC CCG GAG CCG	2043
Met Lys Arg Lys Arg Lys Arg Ala Glu Glu Lys Asp Asp Ala Glu Ala	
620 625 630	
ACG AAC CAG AAC GAA CAG AAT CCG GTG CCG ACA ATG CAT CAC AAT GCG	2091
Arg Lys Glu Asp Glu Glu Asp Ala Val Ala Thr Met His His Asp Gly	
635 640 645 650	
AGT CCG GTG GGT GTA GCT TTG GCT TCA CCG TCT CTC GCG GCG AAA ACT	2139
Ser Gly Val Gly Val Ala Leu Ala Ser Ala Ser Leu Gly Gly Lys Thr	
655 660 665	
GGC ACC AAC ACC GGT CTC ACC TTC GAT GCG GCG AAC CCG AAT ATC ATC	2187
Gly Ser Asp Ser Gly Leu Thr Phe Asp Gly Gly Asp Pro Asp Ile Ile	
670 675 680	
AAA AAC ACC TCC GAC AAC TCC GTC AAC AAC ATT TGT GCC TCA GCA GCA	2235
Lys Asp Thr Trp Asp Lys Ser Val Asp Asp Ile Cys Ala Ser Ala Ala	
685 690 695	
GCA CCG CCG CCG CCG GCA GCA CCG CCG CAC GAG TGT CTC ATG TAC GCG	2283
Ala Ala Ala Ala Ala Ala Ala Ala Ala Asp Glu Cys Leu-Met Tyr Gly	
700 705 710	
GGA TAT CTC CCC TCC GTG CCG GAT AAC AAC AAT CCG AAC TCA GAC TTT	2331
Gly Tyr Val Ala Ser Val Ala Asp Asp Asp Asp Ala Asp Ser Asp Phe	
715 720 725 730	
TGT GTG GGT CCG CTA GAA AAG CCG AAG TCC GAA AAG GAA CTC AAC ACC	2379
Cys Val Ala Pro Leu Glu Arg Ala Lys Ser Glu Lys Glu Leu Asp Thr	
735 740 745	
GAT CCC ACC CTC ATG CAC CCG GGT TCC CCG GCA CCG ACC TCA GCC AAC	2427
Asp Pro Thr Leu Met His Arg Gly Ser Pro Ala Gly Ser Ser Ala Lys	
750 755 760	
GGA CCG TCT CCG GAA GGA CCG GGA CCG CAG GCG AAC AGG ATC TCT	2475
Gly Ala Ser Gly Gly Gly Pro Gly Ala Ala Glu Gly Lys Arg Ile Ser	
765 770 775	
GTT TTA GCG CAG GGT TCC TAC TGT ACC CAG CGT TCG CCC TCG TTC CCG	2523
Val Leu Gly Glu Gly Ser Tyr Cys Ser Glu Arg Trp Pro Ser Leu Ala	
780 785 790	

## FIG. 1 CONT'D.

GCG GCG CCA GTG CCC GGA GCG TGT TCA TCC CAG CTA ATC GCT CCA CCT 2571  
 Ala Ala Gly Val Ala Gly Ala Cys Ser Ser Gln Leu Met Ala Ala Ala  
 795 800 805 810  
 TCG CCA CCG GCG ACC GGA GCG GCG ACC GCG CAA CAG CAG CGA TCC GTG 2619  
 Ser Ala Ala Gly Ser Gly Ala Gly Thr Ala Gln Gln Gln Arg Ser Val  
 815 820 825  
 GTC TCC GCG ACT CCC CAT ATG TAACTCCAAA AATCCCGAAG CCGTCCCTGCT 2670  
 Val Cys Gly Thr Phe His Met  
 830  
 AATCCCGGAG AATCCCGCAT GGAGGAGCTG ACAGGCACATA CACAAAGAAA AGACTGGGTT 2730  
 GCGTTCAAAA TGTGAGAGAG ACCCCAAAAAT GTTCTTTCTTC ATTGAGGCAG TTTAGTCGTC 2790  
 ACCAAAAATG AAAAAATCCT AACCAGGCATA ACTCGTAAAC TCCCTAAAAA ATTGTATAG 2850  
 TAAATTAGCAA AGCTCTGACC CAGCCGTTTC GATCCCGAAT TC 2892

FIG. 2


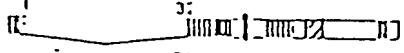




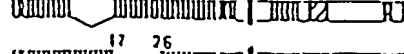
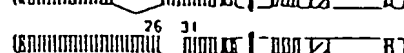

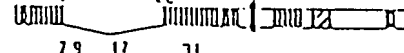
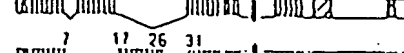

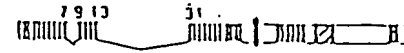
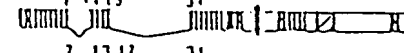
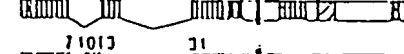
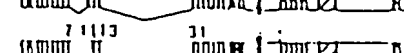

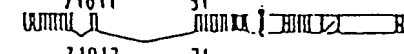
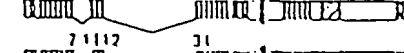


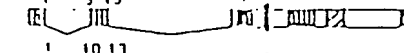
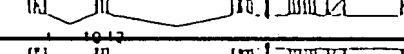
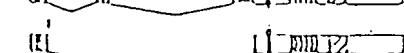
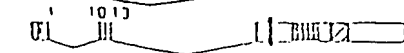
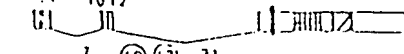



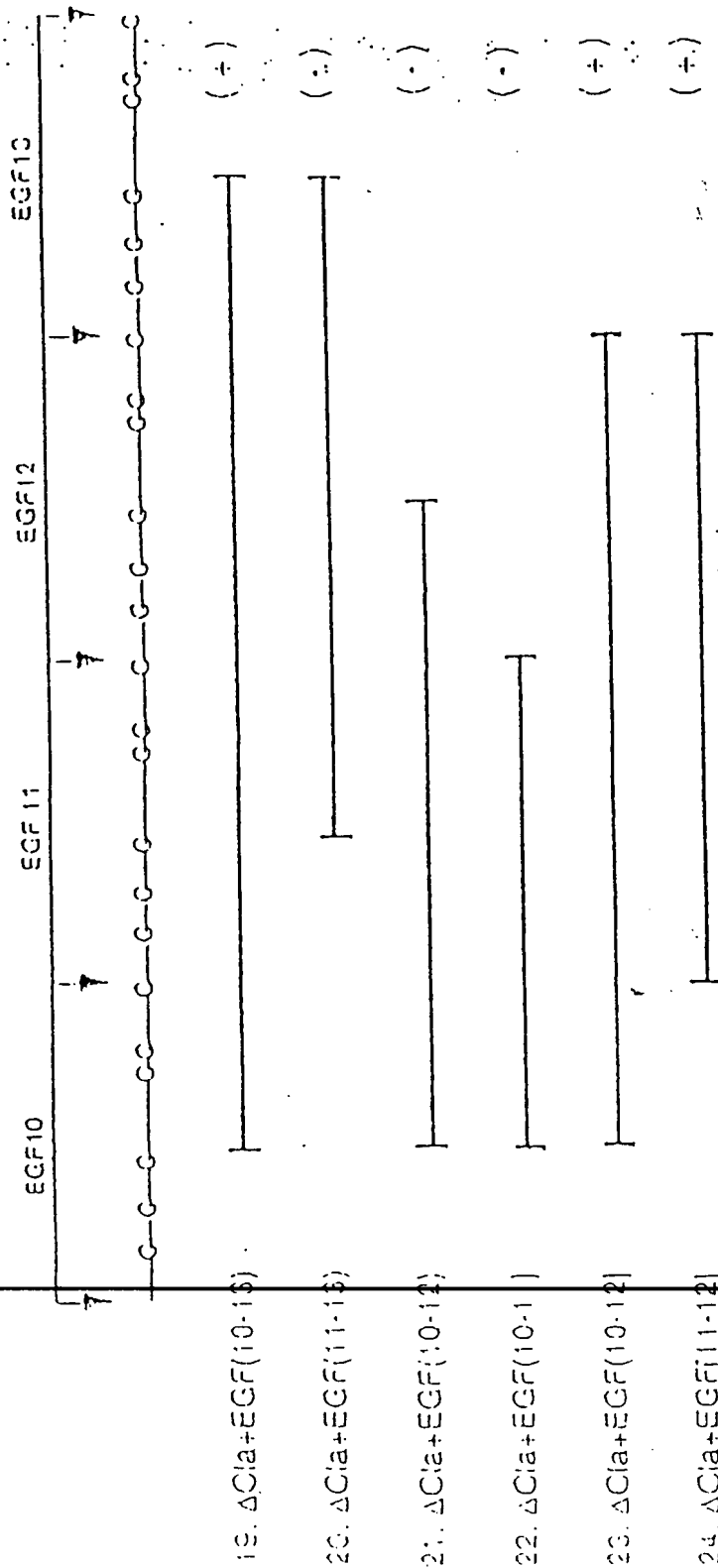
		% Aggregation	
		with DI	with Ser
1. pMINMg		40	21
2. ΔSph		0	nl
3. ΔCln		0	nl
4. ΔEGF(7-17)		0	nl
5. ΔEGF(9-26)		0	nl
6. ΔEGF(17-30)		22	nl
7. ΔEGF(7-9)		20	14
8. ΔEGF(9-17)		0	0
9. ΔEGF(17-26)		10	8
10. ΔEGF(26-30)		5	7
11. ΔEGF(9-30)		0	nl
12. ΔEGF(7-26)		0	nl
13. ΔCln+EGF(9-17)		35	20
14. ΔCln+EGF(17-26)		0	nl
15. split		42	nl
16. ΔCln+EGF(9-13)		47	25
17. ΔCln+EGF(11-15)		0	0
18. ΔCln+EGF(13-17)		0	nl
19. ΔCln+EGF(10-13)		56	23
20. ΔCln+EGF(11-13)		0	nl
21. ΔCln+EGF(10-12)		0	nl
22. ΔCln+EGF(10-11)		0	nl
23. ΔCln+EGF(10-12)		45	nl
24. ΔCln+EGF(11-12)		11	nl
25. ΔEGF		0	nl
26. ΔEGF+EGF(9-17)		24	nl
27. ΔEGF+EGF(9-13)		40	nl
28. ΔEGF+EGF(10-13)		45	23
29. ΔEGF+EGF(10-12)		48	nl
30. ΔECN		0	nl
31. ΔECN+EGF(10-13)		26	nl
32. ΔECN+EGF(10-12)		47	22
33. ΔCln+ΔEGF(10-13)		42	20

FIG. 3



08/532384

FIG. 4

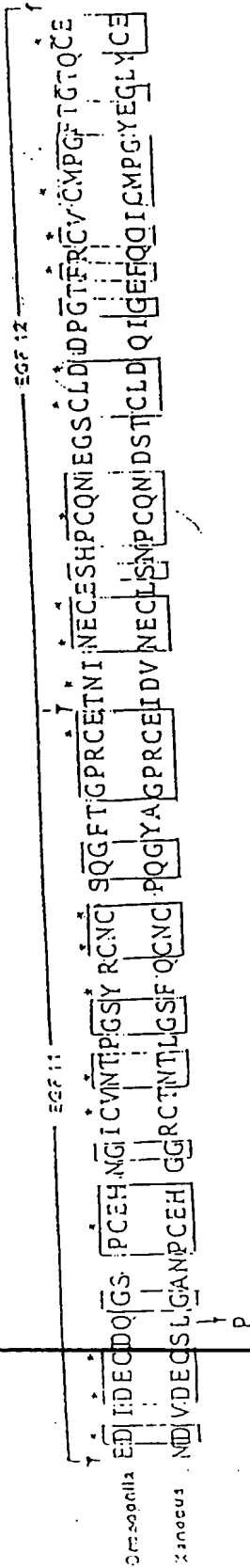


FIG. 5

[illegible]



7326-015 (Sheet 9 of 44)

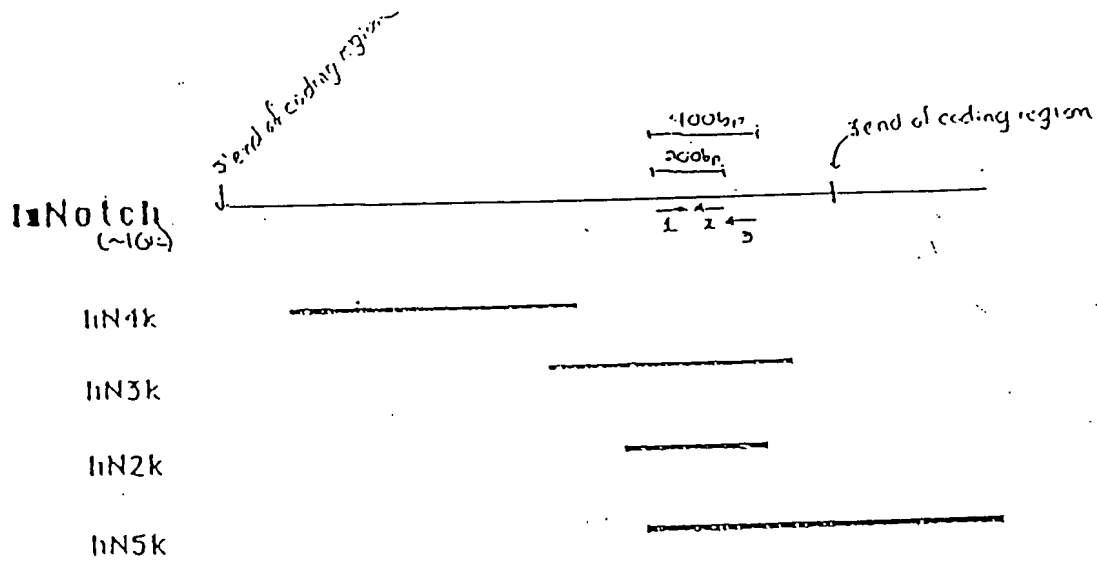
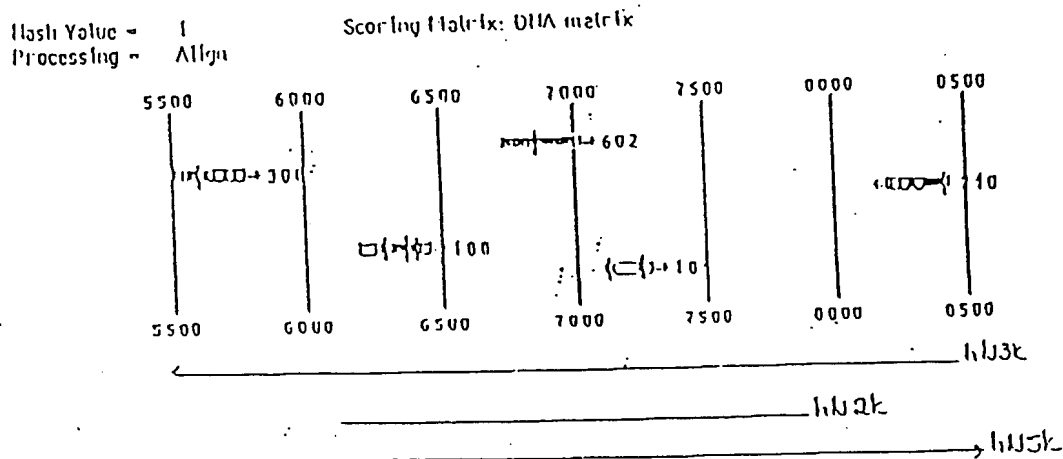
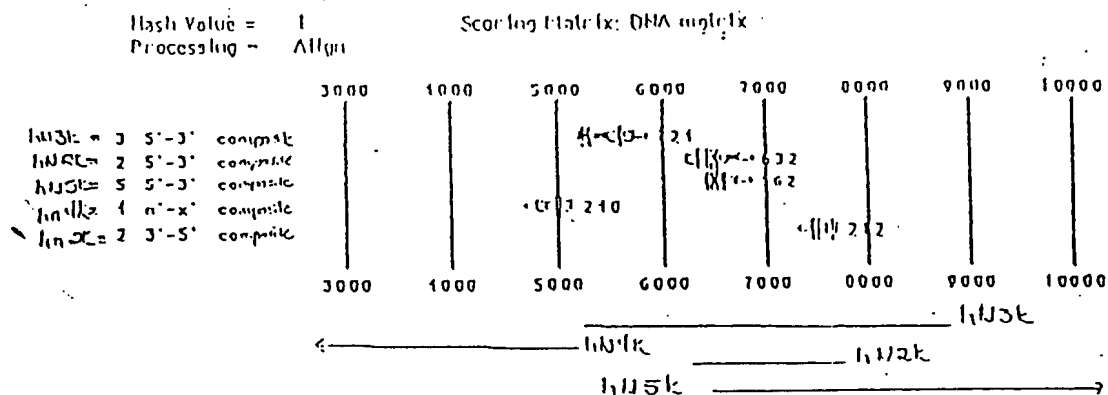


FIG. 6

FIG. 7



7326-015 (Sheet 11 of 44)

## FIG. 8 A-C

A.

```

1  GAAATCCGCT  GGAAGGATGG  TCTGAGCTAC  CTGCCCCGCC  TGCTGGGGCA  TCAATGGCNA
61  GTGGGGGAAA  CCACTCTGGG  CAAACGGGCC  AGGCCATTC  TGAATGTGG  TACATGGTGG
121  GCAAGGGGCC  CGCAGCAGCT  GCAAGGCAGG  TGGACTCAGG  CTGGGGATCC  CCCGCTGDTT
181  GGGCAATAGT  GCCTTTACCC  ATGAGCTGGG  AAGTCACAA  GGGGGGCNAG  GGTCCCCGAG
241  GGCGGTATG  TGCTTCCTTC  AGGTGGC

```

B.

```

1  GAAATCCCTC  CATTATACGT  GACTTTTCTG  AACTGTAGCC  CACCCCTAGTG  TCCTTACCTC
61  CCTCTGGAGT  TTGTCAGCTT  TGGTCTTTTC  AAGAGGCAGG  CTCTCTTCNA  GCTCCTTAA
121  GCGGGCATGC  TCCAGTTTGG  TCTGCGTCTC  AAGATCAGCT  TTGGTAAATG  ATTCTTCTTC
181  AACCCGGGAC  TGAAGGCTGG  CTCTCAGCCCT  CTAGGCAGAG  CAGGAAATTC  GAGGTGGATG
241  TGTTAGATGT  GAATGTCCGT  GGCCAGATG  CCTGCACCCC  ATTGATGTTC  GCTTCTCTCC
301  GAGGAGGCAG  CTCAGATTTG  AGTCATCAGG  ATCAAGATCC  AGAGCACTGT  TCTGCTAACA
361  TCATCAGAGA  CTGGGTCTAC  CAGGGTGCCA  GCCTCCAGHC  CAGACAGACC  GCACTGGTGA
421  GATGGCCCTG  CACCTTGCAG  CCGGTACTTC  ACGGGCTGAT  GCTGCCNAGC  GTCTCCTGGA
481  TGCAGGTGCA  GATGCCAATG  CCCAGGACAA  CATGGGCCGG  TGCCCACTCC  ATGCTGCAGT
541  GGCACGTGAT  GCAAGGTGT  ATTACAGTCT  GTTA

```

C.

```

1  TCCAGATICT  GATTCGCNAC  CGAGTAACTG  ATCTAGATGC  CAGGATGAAT  GATGGTACTA
61  CACCCCTGAT  CCTGGCTGCC  CGCCTGGCTG  TGGAGCGAAT  GGTGGCAGAA  CTGATCAACT
121  GCAAGCGGGA  TGTGAATGCA  GGGATGHC  ATGGAAATTC  TCTCTTCAC  TGGCAGCTG
181  CTGTCATTA  TGAGGGGCA  ACCTTTTCT  TCTTCAAAA  TGGGCGCAAC  CAGACATTC
241  AGGACAGCAA  GCAAGAGACA  CCTCTGTTC  TTGCTGCCCG  GAGGAGCTA  TTAGC

```

## FIG. 9 A-B

A.

```

1  GATTCCTTT  CAGGAGGAAA  GGGTGGGGAG  AGGAGCAGGC  ACCCACTTTC  CCGTGGCTGG
61  ACTCGTTCC  AGGTGGCTCC  ACCGGCAGCT  GTGACCGCCG  CAGGTGGGGG  CGGAGTGCCA
121  TTCAGAAAT  TCCAGAAAG  CCTACCCCA  ACTCGGACGG  CAGGCTCACA  CCGTGGGTG
181  GCAACTGGCA  CACAAACAG  CAGCGTGTCT  GGGGCAAGGG  GGGATGGCAC  CCGTGGAGG
241  CAGAGCTG

```

B.

```

1  CTAAAGGGAA  CAAAGGCHGG  AGCTCCACCC  CGGGCGGCHC  HGCTCTAGAA  CTAGTGGANH
61  HCCCGGGCTG  CAGGAATTC  GGGGAGCTGG  GCTCGGGCTC  AGAGCGGGCG  TGTGGAGAG
121  ATTCTAGACC  GGGAGACCA  GCGATGGCT  GACAGCTGG  CTCCAAAGTC  ACCAGGCTCA
181  NATCGCTGG  CCTGGACATC  GAGGATGCA  GAGGATCAGA  ACCGGTACCT  GATGGGCTG
241  ACTCGGATTT  ACAGGATGA  CAGGCTGCT  TACAGGGAGC  GTGAHNTTT  CACATGAGT
301  CGACAGACAC  GAGCTATG  CAT

```

7326-015 (Sheet 13 of 44)

FIG. 10

10 20 30 40  
 TGC CAG GAG GAC GCG GGC AAC AAG GTC TGC AGC CTG CAG TGC AAC AAC  
 C Q E D A G N K V C S L Q C N N>

50 60 70 80 90  
 CAC GCG TGC GCG TGG GAC GGC GGT GAC TGC TCC CTC AAC TTC AAT GAC  
 H A C G W D G G D C S L N F N D>

100 110 120 130 140  
 CCC TGG AAG AAC TGC ACG CAG TCT CTG CAG TGC TGG AAG TAC TTC AGT  
 P W K N C T Q S L Q C W K Y F S>

150 160 170 180 190  
 GAC GGC CAC TGT GAC AGC CAG TGC AAC TCA GCC GGC TGC CTC TTC GAC  
 D G H C D S Q C N S A G C L F D>

200 210 220 230 240  
 GGC TTT GAC TGC CAG CGT GCG GAA GCC CAG TGC AAC CCC CTG TAC GAC  
 G F D C Q R A E G Q C N P L Y D>

250 260 270 280  
 CAG TAC TGC AAG GAC CAC TTC AGC GAC GGG CAC TGC GAC CAG GGC TGC  
 Q Y C K D H F S D G H C D Q G C>

290 300 310 320 330  
 AAC AGC GCG GAG TGC GAG TGG GAC GGG CTG GAC TGT GCG GAG CAT GTA  
 N S A E C E W D G L D C A E H V>

340 350 360 370 380  
 CCC GAG AAG CTG GCG GCC GGC ACG CTG GTG GTG GTG GTG CTG ATG CCG  
 P E R L A A G T L V V V V L M P>

390 400 410 420 430  
 CCG GAG CAG CTG GCG AAC AGC TCC TTC CAC TTC CTG CCG GAG CTC AGC  
 P E Q L R N S S F H F L R E L S>

440 450 460 470 480  
 CGC GTG CTG CAC ACC AAC GTG GTC TTC AAG CGT GAC GCA CAC GGC CAG  
 R V L H T N V V F K R D A H G Q>

490 500 510 520  
 CAG ATG ATC TTC CCC TAC TAC GGC GGC GAG GAG CAG CTG CCC AAG CAC  
 Q M I F P Y Y G R E E E L R K H>

530 540 550 560 570  
 CCC ATC AAG CGT GCC GCC GAG GGC TGG GCC GCA CCT GAC GCC CTG CTG  
 P I K R A A E G W A A P D A L L>

## FIG. 10 CONT'D

580            590            600            610            620  
 GGC CAG GTG AAG GCC TCG CTG CTC CCT GGT GGC AGC GAG GGT GGG CGG  
 G Q V K A S L L P G G S E G G R>  
 630            640            650            660            670  
 CGG EGG AAG GAG CTG GAG CCC ATG GAC GTC CGC GGC TCC ATC GTC TAC  
 R R R E L D P M D V R G S I V Y>  
 680            690            700            710            720  
 CTG GAG ATT GAC AAC CGG CAG TGT GTG CAG GCC TCC TCG CAG TGC TTC  
 L E I D N R Q C V Q A S S Q C F>  
 730            740            750            760  
 CAG AGT GCC ACC GAC GTG GCC GCA TTC CTG GGA GCG CTC GCC TCG CTG  
 Q S A T D V A A F L G A L A S L>  
 770            780            790            800            810  
 GGC AGC CTC AAC ATC CCC TAC AAG ATC GAG GCC GTG CAG AGT GAG ACC  
 G S L N I P Y K I E A V Q S E T>  
 820            830            840            850            860  
 GTG GAG CCG CCC CCG CCG GCG CAG CTG CAC TTC ATG TAC GTG GCG GCG  
 V E P P P P A Q L H F M Y V A A>  
 870            880            890            900            910  
 GCC GCC TTT GTG CTT CTG TTC TTC GTG GGC TGC GGG GTG CTG CTG TCC  
 A A F V L L F F V G C G V L L S>  
 920            930            940            950            960  
 CGC AAG CGC CCG CCG CAG CAT GGC CAG CTC TGG TTC CCT GAG GGC TTC  
 R K R R R Q H G Q L W F P E G F>  
 970            980            990            1000  
 AAA GTG TCT GAG GCC AGC AAG AAG AAG CCG CCG GAG CCC CTC GGC GAG  
 K V S E A S K K K R R E P L G E>  
 1010            1020            1030            1040            1050  
 GAC TCC GTG GGC CTC AAG CCC CTG AAG AAC GCT TCA GAC GGT GCC CTC  
 D S V G L K P L K N A S D G A L>  
 1060            1070            1080            1090            1100  
 ATG GAC GAC AAC CAG AAT GAG TGG GGG GAC GAG GAC CTG GAG ACC AAG  
 M D D N Q N E W G D E D L E I F>  
 1110            1120            1130            1140            1150  
 AAG TTC CCG TTC GAG GAG CCC GTG GTT CTG CCT GAC CTG GAC GAC CAG  
 K F R F E E P V V L P D L D D Q>  
 1160            1170            1180            1190            1200

## FIG. 10 CONT'D

ACA GAC CAC CGG CAG TGG ACT CAG CAG CAC CTG GAT GCC GCT GAC CTG  
 T D H R Q W T Q Q H L D A A D L>

1210 1220 1230 1240  
 CGC ATG TCT GCC ATG GCC CCC ACA CCG CCC CAG GGT GAG GTT GAC GCC  
 R M S A M A P T P P Q G E V D A>

1250 1260 1270 1280 1290  
 GAC TGC ATG GAC GTC AAT GTC CGC GGG CCT GAT GGC TTC ACC CCG CTC  
 D C M D V N V R G P D G F T P L>

1300 1310 1320 1330 1340  
 ATG ATC GCC TCC TGC AGC GGG GGC GGC CTG GAG ACG GGC AAC AGC GAG  
 M I A S C S G G G L E T G N S E>

1350 1360 1370 1380 1390  
 GAA GAG GAG GAC GCG CCG GCC GTC ATC TCC GAC TTC ATC TAC CAG GGC  
 E E E D A P A V I S D F I Y Q G>

1400 1410 1420 1430 1440  
 GCC AGC CTG CAC AAC CAG ACA GAC CGC ACG GGC GAG ACC GCC TTG CAC  
 A S L H N Q T D R T G E T A L ID>

1450 1460 1470 1480  
 CTG GCC GCC CGC TAC TCA CGC TCT GAT GCC GCC AAG CGC CTG CTG GAG  
 L A A R Y S R S D A A K R L L E>

1490 1500 1510 1520 1530  
 GCC AGC GCA GAT GCC AAC ATC CAG GAG AAC ATG GGC CGC ACC CCG CTG  
 A S A D A N I Q D N M G R T P L>

1540 1550 1560 1570 1580  
 CAT GCG GCT GTG TCT GCC GAC GCA CAA GGT GTC TTC CAG ATC CTG ATC  
 H A A V S A D A Q G V F Q I L ID>

1590 1600 1610 1620 1630  
 CGG AAC CGA GCC ACA GAC CTG GAT GCC CGC ATG CAT GAT GGC ACG ACG  
 R N R A T D L D A R M H D G T T>

1640 1650 1660 1670 1680  
 CCA CTG ATC CTG GCT GCC CGC CTG GCC GTG GAG GGC ATG CTG GAG GAC  
 P L I L A A R L A V E G M L E D>

---

1690 1700 1710 1720  
 CTC ATC AAC TCA CAC GCC GAC GTC AAC GCC GTA GAT GAC CTG GGC AAG  
 L I N S H A D V N A V D D L G E>

1730 1740 1750 1760 1770  
 TCC GCC CTG CAC TGG GCC GCC GCC GTG AAC AAT GTG GAT GCC GCA GTT  
 S A L H W A A A V N H V D A A V>

7326-015 (Sheet 16 of 44)

## FIG. 10 CONT'D

1780	1790	1800	1810	1820
GTG CTC CTG AAG AAC GGG GCT AAC AAA GAT ATG CAG AAC AAC AGG GAG				
V L L K N G A N K D M Q N N R E				
1830	1840	1850	1860	1870
GAG ACA CCC CTG TTT CTG GCC GCC CGG GAG GGC AGC TAC CAG ACC GCC				
E T P L F L A A R E G S Y E T A				
1880	1890	1900	1910	1920
AAG GTG CTG CTG GAC CAC TTT GCC AAC CGG GAC ATC ACG GAT CAT ATG				
K V L L D H F A N R D I T D H M				
1930	1940	1950	1960	
GAC CGC CTG CCG CGC GAC ATC GCA CAG GAG CGC ATG CAT CAC GAC ATC				
D R L P R D I A Q E R M H H D I				
1970	1980	1990	2000	2010
GTG AGG CTG CTG GAC GAG TAC AAC CTG GTG CGC AGC CCG CAG CTG CAC				
V R L L D E Y N L V R S P Q L H				
2020	2030	2040	2050	2060
GGA GCC CCG CTG GGG GGC ACG CCC ACC CTG TCG CCC CCG CTC TGC TCG				
G A P L G G T P T L S P P L C S				
2070	2080	2090	2100	2110
CCC AAC GGC TAC CTG GGC AGC CTC AAG CCC GGC GTG CAG GGC AAG AAG				
P N G Y L G S L K P G V Q G K K				
2120	2130	2140	2150	2160
GTC CGC AAG CCC AGC AGC AAA GGC CTG GCC TGT GGA AGC AAG GAG GCC				
V R K P S S K G L A C G S K E A				
2170	2180	2190	2200	
AAG GAC CTC AAG GCA CGG AAG AAG AAG TCC CAG GAT GGC AAG GGC TGC				
K D L K A R R K K S Q D G K G C				
2210	2220	2230	2240	2250
CTG CTG GAC AGC TCC GGC ATG CTC TCG CCC GTG GAC TCC CTG GAG TCA				
L L D S S G M L S P V D S L E S				
2260	2270	2280	2290	2300
CCC CAT GGC TAC CTG TCA GAC GTG GCC TCG CCG CCA CTG CTG CCC TCC				
P H G Y L S D V A S P P L L P S				
2310	2320	2330	2340	2350
CCG TTC CAG CAG TCT CCG TCC GTG CCC CTC AAC CAC CTG CCT GGG ATG				
P F Q Q S P S V P L R H L P G M				
2360	2370	2380	2390	2400



7326-015 (Sheet 17 of 44)

08/532384

## FIG. 10 CONT'D

CCC GAC ACC CAC CTG GGC ATC GGG CAC CTG AAC GTG GCG GCC AAG CCC  
 P D T H L G I G H L N V A A K P>

2410 2420 2430 2440  
 CAG ATG GCG GCG CTG GGT GGG GGC GGC CGG GTG GCC TTT GAG ACT GGC  
 E M A A L G G G G R L A F E T G>

2450 2460 2470 2480 2490  
 CCA CCT CGT CTC TCC CAC CTG CCT GTG GCC TCT GGC ACC AGC ACC GTC  
 P P R L S H L P V A S G T S T V>

2500 2510 2520 2530 2540  
 CTG GGC TCC AGC AGC GGA GGG GCC CTG AAT TTC ACT GTG GGC GGG TCC  
 L G S S S G G A L N F T V G G S>

2550 2560 2570 2580 2590  
 ACC AGT TTG AAT GGT CAA TGC GAG TGG CTG TCC CGG CTG CAG AGC GGC  
 T S L N G Q C E W L S R L Q S G>

2600 2610 2620 2630 2640  
 ATG GTG CCG AAC CAA TAC AAC CCT CTG CGG GGG AGT GTG GCA CCA GGC  
 M V P N Q Y N P L R G S V A P G>

2650 2660 2670 2680  
 CCC CTG AGC ACA CAG GCC CCC TCC CTG CAG CAT GGC ATG GTA GGC CCG  
 P L S T Q A P S L Q H G M V G P>

2690 2700 2710 2720 2730  
 CTG CAC AGT AGC CTT GCT GCC AGC GCC CTG TCC CAG ATG ATG AGC TAC  
 L H S S L A A S A L S Q M M S Y>

2740 2750 2760 2770 2780  
 CAG GGC CTG CCC AGC ACC CGG CTG GCC ACC CAG CTT CAC CTG GTG CAG  
 Q G L P S T R L A T Q P H L V Q>

2790 2800 2810 2820 2830  
 ACC CAG CAG GTG CAG CCA CAA AAC TTA CAG ATG CAG CAG CAG AAC CTG  
 T Q Q V Q P Q N L Q M Q Q Q N L>

2840 2850 2860 2870 2880  
 CAG GCA GCA AAC ATC CAG CAG CAG CAA AGC CTG CAG CCG CCA CCA CCA  
 Q P A H I Q Q Q Q S L Q P P P P>

2890 2900 2910 2920  
 CCA CCA CAG CCG CAC CTT GGC GTG AGC TCA GCA GCC AGC GGC CAC CTG  
 P P Q F H L G V S S A A S G H I>

2930 2940 2950 2960 2970  
 GGC CGG AGC TTC CTG AGT GGA CAG CCG AGC CAG GCA GAC GTG CAG CCA

## FIG. 10 CONT'D

G R S F L S G E P S Q A D V Q P>

2980 2990 3000 3010 3020

CTG GGC CCC AGC AGC CTG GCG GTG CAC ACT ATT CTG CCC CAG GAG AGC  
 L G P S S L A V H T I L P Q E S>

3030 3040 3050 3060 3070

CCC GCC CTG CCC AGC TCG CTG CCA TCC TCG CTG GTC CCA CCC GTG ACC  
 P A L P T S L P S S L V P P V T>

3080 3090 3100 3110 3120

GCA GCC CAG TTC CTG AGC CCC CCC TCG CAG CAC AGC TAC TCC TCG CCT  
 A A Q F L T P P S Q H S Y S S P>

3130 3140 3150 3160

GTG GAC AAC ACC CCC AGC CAC CAG CTA CAG GTG CCT GTT CCT GTA ATG  
 V D N T P S H Q L Q V P V P V M>

3170 3180 3190 3200 3210

GTA ATG ATC CGA TCT TCG GAT CCT TCT AAA GGC TCA TCA ATT TTG ATC  
 V M I R S S D P S K G S S I L I>

3220 3230

GAA GCT CCC GAC TCA TGG  
 E A P D S W>

## FIG. 11

GAC GTC CAT CTC TTA CAT CTC AAT CTC CGT GCC CCA CAT GCC TGC	46
Glu Val Asp Val Leu Asp Val Asn Val Arg Gly Pro Asp Gly Cys	
1 5 10 15	
ACC CCA TGC ATC TGC GGT TCT CTC CCA CCA GCG AGC TCA CAT TGC ACT	94
Thr Pro Leu Met Leu Ala Ser Leu Arg Gly Gly Ser Ser Asp Leu Ser	
20 25 30	
GAT GAA CAT GAA CAT CCA GAG GAC TCT TCT GGT AAC ATC ATC ACA GAC	142
Asp Glu Asp Glu Asp Ala Glu Asp Ser Ser Ala Asn Ile Ile Thr Asp	
35 40 45	
TTC CTC TAC CAG GGT GCC AAC CTC CAG GCC CAG ACA GAC CGG ACT GGT	190
Leu Val Tyr Glu Gly Ala Ser Leu Glu Ala Glu Thr Asp Arg Thr Gly	
50 55 60	
GAG ATC GCC CTC CAC CTT CCA GCC CGC TAC TCA CCG GCT CAT GCT GCC	238
Glu Met Ala Leu His Leu Ala Ala Arg Tyr Ser Arg Ala Asp Ala Ala	
65 70 75	
AAG CGT CTC CTC GAT CCA GGT CCA CAT GCC AAT GCC CAG GAC AAC ATC	286
Lys Arg Leu Leu Asp Ala Gly Ala Asp Ala Asn Ala Glu Asp Asn Met	
80 85 90 95	
GCC CGC TGT CCA CTC CAT GGT CCA CTC CCA GCT CAT GCC CAA GGT GTC	334
Gly Arg Cys Pro Leu His Ala Ala Val Ala Ala Asp Ala Glu Gly Val	
100 105 110	
TTT CAG ATT CTC ATT CGC AAC CCA GTA ACT GAT GTA GAT GCC AGC ATC	382
Phe Glu Ile Leu Ile Arg Asn Arg Val Thr Asp Leu Asp Ala Arg Met	
115 120 125	
AAT CAT GGT ACT ACA CCC CTC ATC CTC GCT GCC CGC CTC GCT CTC GAG	430
Asn Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala Arg Leu Ala Val Glu	
130 135 140	
GCA ATC GTG CCA GAA CTC ATC AAC TGC CAA GCG CAT GTG AAT CCA GTC	478
Gly Met Val Ala Glu Leu Ile Asn Cys Glu Ala Asp Val Asn Ala Val	
145 150 155	
GAT GAG CAT CCA AAA TCT GGT CTT CAC TGC CCA GCT GCT CTC AAT AAT	526
Asp Asp His Gly Lys Ser Ala Leu His Trp Ala Ala Ala Val Asn Asn	
160 165 170 175	
GTC GAG CCA ACT CTT TTG TTG TTG AAA AAT GCG CCC AAC CCA GAC ATC	574
Val Glu Ala Thr Leu Leu Leu Leu Lys Asn Gly Ala Asn Arg Asp Met	
180 185 190	
CAG GAG AAC AAC GAA CAG ACA GGT CTC TTT CTT GCT CCC CGG GAG GCG	622
Glu Asp Asn Lys Glu Glu Thr Pro Leu Phe Leu Ala Ala Arg Glu Gly	
195 200 205	
AGC TAT GAA CCA GCC AAC ATC CTC TTA GAG CAT TTT GCG AAT CCA GAC	670
Ser Tyr Glu Ala Ala Lys Ile Leu Leu Asp His Phe Ala Asn Arg Asp	
210 215 220	
ATC ACA GAC CAT ATG CAT GGT CTT CCC CGG CAT GTG GCT CGG CAT CGC	718
Ile Thr Asp His Met Asp Arg Leu Pro Arg Asp Val Ala Arg Asp Arg	
225 230 235	
ATC GAG CAT CAC ATT CTC CGC CTT CTC CAT GAA TAC AAT CTC ACC CCA	766
Met His His Asp Ile Val Arg Leu Leu Asp Glu Tyr Asn Val Thr Pro	
240 245 250 255	

## FIG. 11 CONT'D

AGC	CCT	CCA	GGC	ACC	GTC	TTC	ACT	TCT	GCT	CTC	TCA	CCT	GTC	ATC	TGT	014
Ser	Pro	Pro	Gly	Thr	Val	Leu	Thr	Ser	Ala	Leu	Ser	Pro	Val	Ile	Cys	
				260					265					270		
GGC	CCC	AAC	AGA	TCT	TTC	CTC	AGC	CTC	AAG	CAC	ACC	CCA	ATC	CCC	AAC	062
Gly	Pro	Asn	Arg	Ser	Phe	Leu	Ser	Leu	Lys	His	Thr	Pro	Met	Gly	Lys	
			275					280					285			
AAC	TCT	ACN	CCG	CCC	AGT	CCC	AAC	ACT	ACC	ATC	CCT	ACT	AGC	CTC	CCT	910
Lys	Ser	Arg	Arg	Pro	Ser	Ala	Lys	Ser	Thr	Met	Pro	Thr	Ser	Leu	Pro	
			290				295					300				
AAC	CCT	CCC	AAC	GAG	CCA	AAC	GAT	CCC	AAC	CCT	ACT	AGC	AGC	AAC	AAC	950
Asn	Leu	Ala	Lys	Glu	Ala	Lys	Asp	Ala	Lys	Gly	Ser	Asp	Asp	Lys	Lys	
			305			310					315					
TCT	CTC	ACT	GAG	AAG	GTC	CAA	CTC	TCT	GAG	ACT	TCA	GTA	ACT	TTA	TCC	1006
Ser	Leu	Ser	Glu	Lys	Val	Glu	Leu	Ser	Glu	Ser	Ser	Val	Thr	Leu	Ser	
					325					330					335	
CCT	GTT	GAT	TCC	CTA	CAA	TCT	CCT	CAC	ACC	TAT	GTT	TCC	GAG	ACC	ACA	1054
Pro	Val	Asp	Ser	Leu	Glu	Ser	Pro	His	Thr	Tyr	Val	Ser	Asp	Thr	Thr	
				340					345					350		
TCC	TCT	CCA	ATC	ATT	ACA	TCC	CCT	GGC	ATC	TTA	CAG	CCC	TCA	CCC	AAC	1102
Ser	Ser	Pro	Met	Ile	Thr	Ser	Pro	Gly	Ile	Leu	Glu	Ala	Ser	Pro	Asn	
				355				360					365			
CCT	ATC	TTC	CCC	ACT	CCC	CCC	CCT	CCT	CCC	CCA	CTC	CAT	CCC	CAG	CAT	1150
Pro	Met	Leu	Ala	Thr	Ala	Ala	Pro	Pro	Ala	Pro	Val	His	Ala	Glu	His	
				370			375					380				
CCA	CIA	TCT	TTT	TCT	AAC	CTT	CAT	CAA	ATC	CAG	CCT	TTC	CCA	CAT	GGC	1198
Ala	Leu	Ser	Phe	Ser	Asn	Leu	His	Glu	Met	Glu	Pro	Leu	Ala	His	Gly	
				385		390					395					
CCC	ACC	ACT	CTC	CTT	CCC	TCA	CTC	AGC	CAG	TTG	CTA	TCC	CAC	CAC	CAC	1246
Ala	Ser	Thr	Val	Leu	Pro	Ser	Val	Ser	Glu	Leu	Leu	Ser	His	His	His	
					405				410						415	
ATT	CTC	TCT	CCA	GGC	AGT	CCC	AGT	CCT	CCA	AGC	TTG	AGT	AGC	CTC	CAT	1294
Ile	Val	Ser	Pro	Gly	Ser	Gly	Ser	Ala	Gly	Ser	Leu	Ser	Arg	Leu	His	
				420				425						430		
CCA	CTC	CCA	GTC	CCA	CCA	GAT	TGG	ATC	AAC	CCC	ATC	CAG	GTC	AAT	CAG	1342
Pro	Val	Pro	Val	Pro	Ala	Asp	Trp	Met	Asn	Arg	Met	Glu	Val	Asn	Glu	
				435			440						445			
ACC	CAG	TAC	AAT	GAG	ATC	TTT	CCT	ATC	CTC	CTC	GGT	CCA	CCT	GAG	GGC	1390
Thr	Glu	Tyr	Asn	Glu	Met	Phe	Gly	Met	Val	Leu	Ala	Pro	Ala	Glu	Gly	
				450			455					460				
ACC	CAT	CCT	GGC	ATA	CCT	CCC	CAG	AGC	AGC	CCA	CCT	CAA	GGC	AAC	CAC	1438
Thr	His	Pro	Gly	Ile	Ala	Pro	Glu	Ser	Arg	Pro	Pro	Glu	Gly	Lys	His	
				465		470				475						
ATA	ACC	ACC	CCT	GGC	GAG	CCC	TTG	CCC	CCC	ATT	CTC	ACT	TTC	CAG	CTC	1486
Ile	Thr	Thr	Pro	Arg	Glu	Pro	Leu	Pro	Pro	Ile	Val	Thr	Phe	Glu	Leu	
					485			490							495	
ATC	CCT	AAA	GGC	AGT	ATT	CCC	CAA	CCA	GGC	GGC	CCT	CCC	CAG	CCT	CAG	1534
Ile	Pro	Lys	Gly	Ser	Ile	Ala	Glu	Pro	Ala	Gly	Ala	Pro	Glu	Pro	Glu	
				500					505					510		
TCC	ACC	TCC	CCT	CCA	CCT	GTT	CCC	CCC	CCC	CTC	CCC	ACC	ATC	TAC	CAG	1582
Ser	Thr	Cys	Pro	Pro	Ala	Val	Ala	Gly	Pro	Leu	Pro	Thr	Met	Tyr	Glu	
				515			520						525			
ATT	CCA	CAA	ATC	CCT	CCT	TTC	CCC	AGT	CTC	CCT	TTC	CCC	ACT	CCC	ATC	1630
Ile	Pro	Glu	Met	Ala	Arg	Leu	Pro	Ser	Val	Ala	Phe	Pro	Thr	Ala	Met	
				530			535						540			

## FIG. // CONT'D

ATG CCC CAG CAG CAG GGG CAG GTA GCT CAG ACC ATT CTC CCA GCC TAT Met Pro Gln Gln Asp Gly Gln Val Ala Gln Thr Ile Leu Pro Ala Tyr 545 550 555	1678
CAT CCT ATC CCA GCG TCT GTG GGC AAG TAC CCC ACA CCC CCT TCA CAG His Pro Phe Pro Ala Ser Val Gly Tyr Tyr Pro Thr Pro Pro Ser Gln 560 565 570 575	1726
CAC AGT TAT CCT TCC TCA AAT GCT GCT GAG CGA ACA CCC AGT CAG AGT His Ser Tyr Ala Ser Ser Asn Ala Ala Gln Arg Thr Pro Ser His Ser 580 585 590	1774
GGT CAC CTC CAG GGT GAG CAT CCC TAC CTG ACA CCA TCC CCA GAG TCT Gly His Leu Gln Gly Gln His Pro Tyr Leu Thr Pro Ser Pro Gln Ser 595 600 605	1822
CCT GAG CAG TGG TCA AGT TCA TCA CCC CAG TCT GCT TCT GAG TGG TCA Pro Asp Gln Trp Ser Ser Ser Ser Pro His Ser Ala Ser Asp Trp Ser 610 615 620	1870
CAT GTG ACC ACC ACC CCT ACC CCT GGG GGT GCT GGA GGA GGT CAG CCG Asp Val Thr Thr Ser Pro Thr Pro Gly Gly Ala Gly Gly Gly Gln Arg 625 630 635	1918
GGA CCT GGG ACA CAC ATG TCT GAG CCA CCA CAC AAC AAC ATG CAG GTT Gly Pro Gly Thr His Met Ser Gln Pro Pro His Asn Asn Met Gln Val 640 645 650 655	1966
TAT GCG TGGAGAGTTC CACCTCCAGT GTAGAGACAT AACTGACTTT TGTAAATGCT Tyr Ala	2022
GGTACGAAAC AAATGAAAGT CATCCGGGAG AGAAATGAAAC AAATCTCTGG ACCCAGCTTC	2082
TAGAGGTAGG AAAGAGAAAG TGTCTTATT CAGATAATGC AACAGAAAGCA ATTGCTCAGT	2142
TTCATCTGGT ATCTGCAAAG CTTATTGATT ATTCTAATCT AATAAGACAA GTTGTGGAA	2202
ATGCAAGATC AATACAAAGC TTGGGTCCAT GTTACCTCTC TTCTATTGG AGAATAAGAT	2262
GGATGCTAT TGAAGCCCCAG ACATTCTTGC AGCTTGGACT GCATTTTAAAG CCTTGCAGGC	2322
TTCTGCCATA TCCATGAGAA GATTCTACAC TAGCGTCTCT TTGGCAATTA TCCCTCGAA	2382
TTCTGCCATG ATTGACCTAC GCATCTCTCT CTCCCTGGAG ATTCTTTTGT GTTCATTGG	2442
TGCTTTTGGT TTTCACCTCT TCCGTGATTG TACCCCTACC AGCATGTTAT AGGGCAGAGC	2502
CTTTGTGCTT TTGATCAATC TGGCCCATGA AAGCAACTTT GGTCTCCTTT CCCCTCCTGT	2562
CTTCCCGGTA TCCCTTGGAG TCTCAAAAGG TTTACTTTGG TATGGTCTCT AGCACAAGAC	2622
TTTCAAGTAT GTTGTTTCTT TGGAAAATGG ACATACCTGA TTGTGTCTCT CTGCATATAT	2682
CATTCTTGA CAGAGAAAGG GAGAAAGATA CTTTCTTCA ACAAATTTTG CCGGCAGGAG	2742
ATCCCTTCAA CAGGCTGCAC CTTAATTTTT CTGTCTGTGT TCCAGGTCTT CATATAAACT	2802
TTACCAAGGA CAAAGGCTGT AGTTTGTGT TTTCTCTGT ATCCGCTCTG TCACTGTAAA	2862
GTTTTATCCT TCAATGCTTA GTTACTAAGA CCTCCCCAC TTTTAAAAA CCAAGAAAAAG	2922
GTTCGAATG TTGCAATGAC CAAAGAGCAA GTTAATCTGT CCAAGAGCCA GTTACCCACC	2982
CACAGGTCCC CCACTTCTCT GGCAGGCATT CCAATGACTC CCTGTATGGA ACACATTTGT	3042
CCCAGATCTG ACCATTCTAG GCTCTTTTCA CTCACCTACC CAGCAATGCA AACATGCTT	3102
AACCTGTGAG CTTTCTCTT CATACTCACA GAAAGAGCTC TCTCAAAATG TCAACCTTCT	3162

## FIG. 11 CONT'D

CCATTTACGA CTGAACCTTC CTTAGCCCAA GGGACCCACT GACAGTGTG TTCCGTTTGT 3222  
 CAGATGATCA GTCTCTACTG ATTATCTTGC TGCTTAAGG CCCTGTCACC AATCTTTCTT 3282  
 TCACACCGTG TGGTCCGCTG TACTGGTATA CCCAGTATCT TCTCAGTCGA GACATGGACT 3342  
 TTATATGTTG AAGTCCACGA ATTCCAAAGT TCCAGTCTCT TTCTATGATC CAAAACAGCC 3402  
 CTATAAGAA GCTTGCAGAA GAGCAACTAT ATAGCACCCCT TTCTATTTT CTGCTACCAT 3462  
 TTCTTTTCTT CTGAAGCCGC CATGACATTC CCTTTGCCAA CTAACTAGCA AACTCAGCAG 3522  
 AACATTTTCC TTTCCTAGAG TCACCTTTTA GATGATAATG GACAACTATA GACTTGGTCA 3582  
 TTGTTCAAGC TGATTGCCCC TCACCTGAAT CCAGTCTCTG TATTATGCT CTTCGCCATT 3642  
 TCTTTCACTT TCTTTTAAAG CCAGAAACAT TTTAGTTAAT TGTAGATAAA GAATAGTTTT 3702  
 CTTCCTCTTC TCCTTGGGCC ACTTAATAAT TGGTCCATCG CTACAGTCCA ACTTCCGTCC 3762  
 AGTGGTCTGA TCCCCATGAC ACCTGCCAAA TAAGTTCTCG CTGGCCATT TGTAGATATT 3822  
 AACAGGTGAA TTCCCGACTC TTTTGGTTTG AATGACAGTT CTCATTCCCT CTATGGCTGC 3882  
 AAGTATGCAT CAGTGCCTCC CACTTACCTG ATTTGTCTGT CGGTGGCCCC ATATGGAAAC 3942  
 CCTGCGTCTC TGTTGGCATA ATAGTTTACA AATGGTTTTT TCAGTCCCTAT CCAATTTTAT 4002  
 TGAACCAACA AAAATAATTA CTTCGCCCC GAGATAAGCA GATTAAGTTT GTTCATTCTC 4062  
 TGCTTTATTC TCTCCATGTG GCAACATTCT CTCAGCCTCT TTCTATGCTG GCAACATTT 4122  
 TATCATTTCTA AATGGTCACT CTCGCCCCCT GGACCCATT ATTATTACA GATGGGGAGA 4182  
 ACCTATCTGC ATGGACCCCT ACCATCCTCT GTGCAGCACA CACAGTGCAG GGAGCCAGTG 4242  
 GCGATGCGCA TCACTTTCTT CCCCCTG 4268

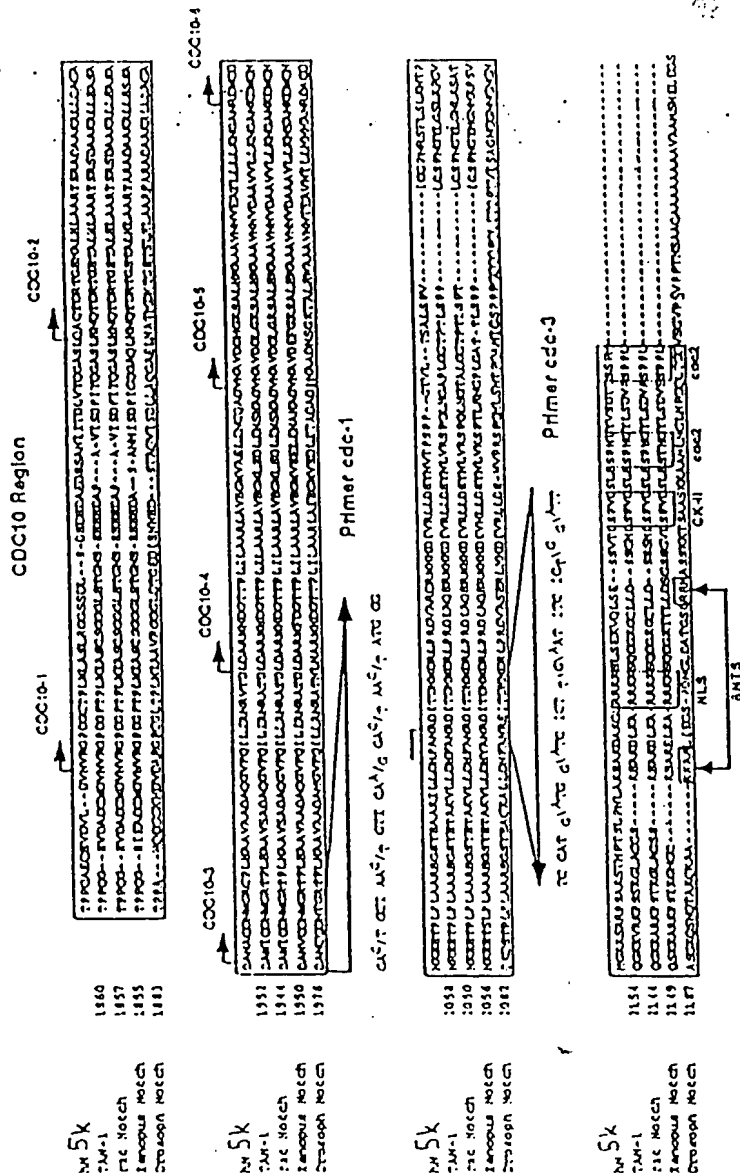


FIG. 12 A-B

[illegible]

1-11-71  
K5

11310 ..... 11311 11312 11313 11314 11315 11316 11317 11318 11319 11320 11321 11322 11323 11324 11325 11326 11327 11328 11329 11330 11331 11332 11333 11334 11335 11336 11337 11338 11339 11340 11341 11342 11343 11344 11345 11346 11347 11348 11349 11350 11351 11352 11353 11354 11355 11356 11357 11358 11359 11360 11361 11362 11363 11364 11365 11366 11367 11368 11369 11370 11371 11372 11373 11374 11375 11376 11377 11378 11379 11380 11381 11382 11383 11384 11385 11386 11387 11388 11389 11390 11391 11392 11393 11394 11395 11396 11397 11398 11399 11400 11401 11402 11403 11404 11405 11406 11407 11408 11409 11410 11411 11412 11413 11414 11415 11416 11417 11418 11419 11420 11421 11422 11423 11424 11425 11426 11427 11428 11429 11430 11431 11432 11433 11434 11435 11436 11437 11438 11439 11440 11441 11442 11443 11444 11445 11446 11447 11448 11449 11450 11451 11452 11453 11454 11455 11456 11457 11458 11459 11460 11461 11462 11463 11464 11465 11466 11467 11468 11469 11470 11471 11472 11473 11474 11475 11476 11477 11478 11479 11480 11481 11482 11483 11484 11485 11486 11487 11488 11489 11490 11491 11492 11493 11494 11495 11496 11497 11498 11499 11500 11501 11502 11503 11504 11505 11506 11507 11508 11509 11510 11511 11512 11513 11514 11515 11516 11517 11518 11519 11520 11521 11522 11523 11524 11525 11526 11527 11528 11529 11530 11531 11532 11533 11534 11535 11536 11537 11538 11539 11540 11541 11542 11543 11544 11545 11546 11547 11548 11549 11550 11551 11552 11553 11554 11555 11556 11557 11558 11559 11560 11561 11562 11563 11564 11565 11566 11567 11568 11569 11570 11571 11572 11573 11574 11575 11576 11577 11578 11579 11580 11581 11582 11583 11584 11585 11586 11587 11588 11589 11590 11591 11592 11593 11594 11595 11596 11597 11598 11599 11600 11601 11602 11603 11604 11605 11606 11607 11608 11609 11610 11611 11612 11613 11614 11615 11616 11617 11618 11619 11620 11621 11622 11623 11624 11625 11626 11627 11628 11629 11630 11631 11632 11633 11634 11635 11636 11637 11638 11639 11640 11641 11642 11643 11644 11645 11646 11647 11648 11649 11650 11651 11652 11653 11654 11655 11656 11657 11658 11659 11660 11661 11662 11663 11664 11665 11666 11667 11668 11669 11670 11671 11672 11673 11674 11675 11676 11677 11678 11679 11680 11681 11682 11683 11684 11685 11686 11687 11688 11689 11690 11691 11692 11693 11694 11695 11696 11697 11698 11699 11700 11701 11702 11703 11704 11705 11706 11707 11708 11709 11710 11711 11712 11713 11714 11715 11716 11717 11718 11719 11720 11721 11722 11723 11724 11725 11726 11727 11728 11729 11730 11731 11732 11733 11734 11735 11736 11737 11738 11739 11740 11741 11742 11743 11744 11745 11746 11747 11748 11749 11750 11751 11752 11753 11754 11755 11756 11757 11758 11759 11760 11761 11762 11763 11764 11765 11766 11767 11768 11769 11770 11771 11772 11773 11774 11775 11776 11777 11778 11779 11780 11781 11782 11783 11784 11785 11786 11787 11788 11789 11790 11791 11792 11793 11794 11795 11796 11797 11798 11799 11800 11801 11802 11803 11804 11805 11806 11807 11808 11809 11810 11811 11812 11813 11814 11815 11816 11817 11818 11819 11820 11821 11822 11823 11824 11825 11826 11827 11828 11829 11830 11831 11832 11833 11834 11835 11836 11837 11838 11839 11840 11841 11842 11843 11844 11845 11846 11847 11848 11849 11850 11851 11852 11853 11854 11855 11856 11857 11858 11859 11860 11861 11862 11863 11864 11865 11866 11867 11868 11869 11870 11871 11872 11873 11874 11875 11876 11877 11878 11879 11880 11881 11882 11883 11884 11885 11886 11887 11888 11889 11890 11891 11892 11893 11894 11895 11896 11897 11898 11899 11900 11901 11902 11903 11904 11905 11906 11907 11908 11909 11910 11911 11912 11913 11914 11915 11916 11917 11918 11919 11920 11921 11922 11923 11924 11925 11926 11927 11928 11929 11930 11931 11932 11933 11934 11935 11936 11937 11938 11939 11940 11941 11942 11943 11944 11945 11946 11947 11948 11949 11950 11951 11952 11953 11954 11955 11956 11957 11958 11959 11960 11961 11962 11963 11964 11965 11966 11967 11968 11969 11970 11971 11972 11973 11974 11975 11976 11977 11978 11979 11980 11981 11982 11983 11984 11985 11986 11987 11988 11989 11990 11991 1

245k  
 244-1  
 243 2020  
 242 2020  
 241 2020

[illegible]

5k  
 1M-1  
 12M-1  
 12M-1  
 12M-1

המחלקה הכלכלית והסטטיסטית

5k  
TAM-1  
FAC MOLEN  
FAC MOLEN  
STATION MOLEN

**PEST-containing Region**

FIG. 12B CONT'D



FIG. 13

Potential signal cleavage site  
EGF-like Repeats

Hum H	33	-----ALRAL LVALALMLC CA-----APA HA-----	QCRDQYEVY NGRNVTYHN OTYOKCPDS FLGEXCOHRD PCE-KNRCON GGTC--VAQA
TAN-1	30	-----PL LAPLALALL PA-----LAA RG-----	PCSPGQDPA FVPRGCDPN PCL-STPKAN AGTCHVDDR
Xen H	20	-----RIGLAVILCS LP-----VLT QG-----	RCSTQATBCL NGRCRCHTP OTYGLCAOLH
Dros H	117	-----RAPHVWICPM INKHAVSL PASPLULLT LAFANLPHV RGTOTALVH	YTERICQTPN PCTIKRQCHN FOTCEPVLQD
		-----SCTSV--CQ NGDTEVTQLN QRTYKACDSH	PCN-SHRCN FOTCEVTFRH
Hum H	159	-----PCLANGTCHH LSRT-YECT CQVGTGKEC QMTDACLSPH CANOCTCTTV	--ANQFSCIK LTFOTQKCE TQVNEC-DIP GHQHGQTCGL
TAN-1	136	-----PLDNAC-LTN PCRNQGTCHL LT-LTEYKCR CPFGHGXKSC QMADPCASNP CANOCCCLPF	--EASVYCHC PPFHIOPTCR QVNEGCKPK RLCHRGQTCGL
Xen H	136	-----PVDNAC-VNN PCRNQGTCHL LNSVTEYKCR CPFGHGXKSC QMADPCASNP CANOCCCLPF	--EASVYCHC PPFHIOPTCR QVNEGCKPK RLCHRGQTCGL
Dros H	222	-----AVPHAC-DHV TCLANGTCTOL KT-LEEYVCA CANOYTGRC ETRNLCASSP CENAGTCTAL	AQSSFTCSG PPFOTGDTCS YDIEEC-Q-S NPKYGGCTEV
Hum H	312	-----SLVPCAPSP CVNGGTCTGRT GDTTECNCL POFEGSTCR NIDCCPHIRC QNGGVCVDGV	MTYNCRPPQ WTCQCTEDV DECLQAPNA - CONGCTCANR
TAN-1	315	-----RPVPCSPSP CONGCTCTRT DQSYTHCACL POFQGNCEE NIDCCPHIRC QNGGVCVDGV	MTYNCRPPQ WTCQCTEDV DECLQAPNA - CONGCTCANR
Xen H	314	-----CLNVPCHSP CLNVPCHSP CLNVPCHSP CLNVPCHSP CLNVPCHSP	MTYNCRPPQ WTCQCTEDV DECLQAPNA - CONGCTCANR
Dros H	352	-----TYNFCSPSP CONAGICRSH G-LSYCKCP KGFEDKNCED NYDCLAHLC QNGGTCIDGI	SDYTCRPPN FTGRQCQDDV DECAQRDHPV CONGCTCTMT
Hum H	433	-----IDCCAFASCT PGSTCIDRVA SFSNCPBEX AGLLCHLDDA CTSNCPHKA	LCDNPLAQ YICTCPQYK GADCTEDVE CANANSNPE HAGKCVNTDG
TAN-1	434	-----IDCCAFASCT PGSTCIDRVA SFSNCPBEX AGLLCHLDDA CTSNCPHKA	LCDNPLAQ YICTCPQYK GADCTEDVE CANANSNPE HAGKCVNTDG
Xen H	433	-----IDCCAFASCT PGSTCIDRVA SFSNCPBEX AGLLCHLDDA CTSNCPHKA	LCDNPLAQ YICTCPQYK GADCTEDVE CANANSNPE HAGKCVNTDG
Dros H	476	-----IDCCAFASCT PGSTCIDRVA SFSNCPBEX AGLLCHLDDA CTSNCPHKA	LCDNPLAQ YICTCPQYK GADCTEDVE CANANSNPE HAGKCVNTDG
Hum H	552	-----ECHSDPCQND ATCLDKIOGF TGLCHPRTG VHCLEINSC QSNPCVNGQ	CVKVRRTQC LPPMFTYBP CQIDIDCCS TPCLNQAKCI DHPNGYECOC
TAN-1	554	-----ECVSNPCQND ATCLDKIOGF TGLCHPRTG VHCLEINSC QSNPCVNGQ	CVKVRRTQC LPPMFTYBP CQIDIDCCS TPCLNQAKCI DHPNGYECOC
Xen H	553	-----ECVSNPCQND ATCLDKIOGF TGLCHPRTG VHCLEINSC QSNPCVNGQ	CVKVRRTQC LPPMFTYBP CQIDIDCCS TPCLNQAKCI DHPNGYECOC
Dros H	596	-----ECVSNPCQND ATCLDKIOGF TGLCHPRTG VHCLEINSC QSNPCVNGQ	CVKVRRTQC LPPMFTYBP CQIDIDCCS TPCLNQAKCI DHPNGYECOC
Hum H	677	-----DSTYTCINRG PVALICSDQI DCTYSSPCLN DGRCDILVNG YQNCNCPOTS	GVNCEINFD CASNPCHG- ICHMDINRYS CVCSPPQTCQ
TAN-1	673	-----DSTYTCINRG PVALICSDQI DCTYSSPCLN DGRCDILVNG YQNCNCPOTS	GVNCEINFD CASNPCHG- ICHMDINRYS CVCSPPQTCQ
Xen H	672	-----DSTYTCINRG PVALICSDQI DCTYSSPCLN DGRCDILVNG YQNCNCPOTS	GVNCEINFD CASNPCHG- ICHMDINRYS CVCSPPQTCQ
Dros H	716	-----DSTYTCINRG PVALICSDQI DCTYSSPCLN DGRCDILVNG YQNCNCPOTS	GVNCEINFD CASNPCHG- ICHMDINRYS CVCSPPQTCQ
Hum H	777	-----DSTYTCINRG PVALICSDQI DCTYSSPCLN DGRCDILVNG YQNCNCPOTS	GVNCEINFD CASNPCHG- ICHMDINRYS CVCSPPQTCQ
TAN-1	752	-----DSTYTCINRG PVALICSDQI DCTYSSPCLN DGRCDILVNG YQNCNCPOTS	GVNCEINFD CASNPCHG- ICHMDINRYS CVCSPPQTCQ
Xen H	731	-----DSTYTCINRG PVALICSDQI DCTYSSPCLN DGRCDILVNG YQNCNCPOTS	GVNCEINFD CASNPCHG- ICHMDINRYS CVCSPPQTCQ
Dros H	875	-----DSTYTCINRG PVALICSDQI DCTYSSPCLN DGRCDILVNG YQNCNCPOTS	GVNCEINFD CASNPCHG- ICHMDINRYS CVCSPPQTCQ
Hum H	914	-----DSTYTCINRG PVALICSDQI DCTYSSPCLN DGRCDILVNG YQNCNCPOTS	GVNCEINFD CASNPCHG- ICHMDINRYS CVCSPPQTCQ
TAN-1	911	-----DSTYTCINRG PVALICSDQI DCTYSSPCLN DGRCDILVNG YQNCNCPOTS	GVNCEINFD CASNPCHG- ICHMDINRYS CVCSPPQTCQ
Xen H	909	-----DSTYTCINRG PVALICSDQI DCTYSSPCLN DGRCDILVNG YQNCNCPOTS	GVNCEINFD CASNPCHG- ICHMDINRYS CVCSPPQTCQ
Dros H	949	-----DSTYTCINRG PVALICSDQI DCTYSSPCLN DGRCDILVNG YQNCNCPOTS	GVNCEINFD CASNPCHG- ICHMDINRYS CVCSPPQTCQ
Hum H	1014	-----DSTYTCINRG PVALICSDQI DCTYSSPCLN DGRCDILVNG YQNCNCPOTS	GVNCEINFD CASNPCHG- ICHMDINRYS CVCSPPQTCQ
TAN-1	1011	-----DSTYTCINRG PVALICSDQI DCTYSSPCLN DGRCDILVNG YQNCNCPOTS	GVNCEINFD CASNPCHG- ICHMDINRYS CVCSPPQTCQ
Xen H	1029	-----DSTYTCINRG PVALICSDQI DCTYSSPCLN DGRCDILVNG YQNCNCPOTS	GVNCEINFD CASNPCHG- ICHMDINRYS CVCSPPQTCQ
Dros H	1059	-----DSTYTCINRG PVALICSDQI DCTYSSPCLN DGRCDILVNG YQNCNCPOTS	GVNCEINFD CASNPCHG- ICHMDINRYS CVCSPPQTCQ
Hum H	1154	-----DSTYTCINRG PVALICSDQI DCTYSSPCLN DGRCDILVNG YQNCNCPOTS	GVNCEINFD CASNPCHG- ICHMDINRYS CVCSPPQTCQ
TAN-1	1151	-----DSTYTCINRG PVALICSDQI DCTYSSPCLN DGRCDILVNG YQNCNCPOTS	GVNCEINFD CASNPCHG- ICHMDINRYS CVCSPPQTCQ
Xen H	1149	-----DSTYTCINRG PVALICSDQI DCTYSSPCLN DGRCDILVNG YQNCNCPOTS	GVNCEINFD CASNPCHG- ICHMDINRYS CVCSPPQTCQ
Dros H	1168	-----DSTYTCINRG PVALICSDQI DCTYSSPCLN DGRCDILVNG YQNCNCPOTS	GVNCEINFD CASNPCHG- ICHMDINRYS CVCSPPQTCQ

1361 hum N  
 1362 TAN-1  
 1363 XEN N  
 1364 DROS N  
 1365  
 1366  
 1367  
 1368  
 1369  
 1370  
 1371  
 1372  
 1373  
 1374  
 1375  
 1376  
 1377  
 1378  
 1379  
 1380  
 1381  
 1382  
 1383  
 1384  
 1385  
 1386  
 1387  
 1388  
 1389  
 1390  
 1391  
 1392  
 1393  
 1394  
 1395  
 1396  
 1397  
 1398  
 1399  
 1400  
 1401  
 1402  
 1403  
 1404  
 1405  
 1406  
 1407  
 1408  
 1409  
 1410  
 1411  
 1412  
 1413  
 1414  
 1415  
 1416  
 1417  
 1418  
 1419  
 1420  
 1421  
 1422  
 1423  
 1424  
 1425  
 1426  
 1427  
 1428  
 1429  
 1430  
 1431  
 1432  
 1433  
 1434  
 1435  
 1436  
 1437  
 1438  
 1439  
 1440  
 1441  
 1442  
 1443  
 1444  
 1445  
 1446  
 1447  
 1448  
 1449  
 1450  
 1451  
 1452  
 1453  
 1454  
 1455  
 1456  
 1457  
 1458  
 1459  
 1460  
 1461  
 1462  
 1463  
 1464  
 1465  
 1466  
 1467  
 1468  
 1469  
 1470  
 1471  
 1472  
 1473  
 1474  
 1475  
 1476  
 1477  
 1478  
 1479  
 1480  
 1481  
 1482  
 1483  
 1484  
 1485  
 1486  
 1487  
 1488  
 1489  
 1490  
 1491  
 1492  
 1493  
 1494  
 1495  
 1496  
 1497  
 1498  
 1499  
 1500  
 1501  
 1502  
 1503  
 1504  
 1505  
 1506  
 1507  
 1508  
 1509  
 1510  
 1511  
 1512  
 1513  
 1514  
 1515  
 1516  
 1517  
 1518  
 1519  
 1520  
 1521  
 1522  
 1523  
 1524  
 1525  
 1526  
 1527  
 1528  
 1529  
 1530  
 1531  
 1532  
 1533  
 1534  
 1535  
 1536  
 1537  
 1538  
 1539  
 1540  
 1541  
 1542  
 1543  
 1544  
 1545  
 1546  
 1547  
 1548  
 1549  
 1550  
 1551  
 1552  
 1553  
 1554  
 1555  
 1556  
 1557  
 1558  
 1559  
 1560  
 1561  
 1562  
 1563  
 1564  
 1565  
 1566  
 1567  
 1568  
 1569  
 1570  
 1571  
 1572  
 1573  
 1574  
 1575  
 1576  
 1577  
 1578  
 1579  
 1580  
 1581  
 1582  
 1583  
 1584  
 1585  
 1586  
 1587  
 1588  
 1589  
 1590  
 1591  
 1592  
 1593  
 1594  
 1595  
 1596  
 1597  
 1598  
 1599  
 1600  
 1601  
 1602  
 1603  
 1604  
 1605  
 1606  
 1607  
 1608  
 1609  
 1610  
 1611  
 1612  
 1613  
 1614  
 1615  
 1616  
 1617  
 1618  
 1619  
 1620  
 1621  
 1622  
 1623  
 1624  
 1625  
 1626  
 1627  
 1628  
 1629  
 1630  
 1631  
 1632  
 1633  
 1634  
 1635  
 1636  
 1637  
 1638  
 1639  
 1640  
 1641  
 1642  
 1643  
 1644  
 1645  
 1646  
 1647  
 1648  
 1649  
 1650  
 1651  
 1652  
 1653  
 1654  
 1655  
 1656  
 1657  
 1658  
 1659  
 1660  
 1661  
 1662  
 1663  
 1664  
 1665  
 1666  
 1667  
 1668  
 1669  
 1670  
 1671  
 1672  
 1673  
 1674  
 1675  
 1676  
 1677  
 1678  
 1679  
 1680  
 1681  
 1682  
 1683  
 1684  
 1685  
 1686  
 1687  
 1688  
 1689  
 1690  
 1691  
 1692  
 1693  
 1694  
 1695  
 1696  
 1697  
 1698  
 1699  
 1700  
 1701  
 1702  
 1703  
 1704  
 1705  
 1706  
 1707  
 1708  
 1709  
 1710  
 1711  
 1712  
 1713  
 1714  
 1715  
 1716  
 1717  
 1718  
 1719  
 1720  
 1721  
 1722  
 1723  
 1724  
 1725  
 1726  
 1727  
 1728  
 1729  
 1730  
 1731  
 1732  
 1733  
 1734  
 1735  
 1736  
 1737  
 1738  
 1739  
 1740  
 1741  
 1742  
 1743  
 1744  
 1745  
 1746  
 1747  
 1748  
 1749  
 1750  
 1751  
 1752  
 1753  
 1754  
 1755  
 1756  
 1757  
 1758  
 1759  
 1760  
 1761  
 1762  
 1763  
 1764  
 1765  
 1766  
 1767  
 1768  
 1769  
 1770  
 1771  
 1772  
 1773  
 1774  
 1775  
 1776  
 1777  
 1778  
 1779  
 1780  
 1781  
 1782  
 1783  
 1784  
 1785  
 1786  
 1787  
 1788  
 1789  
 1790  
 1791  
 1792  
 1793  
 1794  
 1795  
 1796  
 1797  
 1798  
 1799  
 1800  
 1801  
 1802  
 1803  
 1804  
 1805  
 1806  
 1807  
 1808  
 1809  
 1810  
 181

2235	-----	PLANCASV	LPSVSQLLSH	HHIVSPGS--	2235
2306	-----	LPVASCSTV	LOSSSGALN	FTVOCSTSLN	2306
2394	-----	L-NASSPNTI	MS--	NGSNH	2394
2445	-----	FTDMVRUTH	SSIALSPHAY	LQSPSPAKSR	2445
2320	-----	SHQGLSACGN	SHQGLSACGN	SHQGLSACGN	2320
2414	-----	QQLQNPANTO	QQLQNPANTO	QQLQNPANTO	2414
2384	-----	QQLQNPANTO	QQLQNPANTO	QQLQNPANTO	2384
2565	-----	QQLQNPANTO	QQLQNPANTO	QQLQNPANTO	2565
2433	-----	QQLQNPANTO	QQLQNPANTO	QQLQNPANTO	2433
2530	-----	QQLQNPANTO	QQLQNPANTO	QQLQNPANTO	2530
2497	-----	QQLQNPANTO	QQLQNPANTO	QQLQNPANTO	2497
2671	-----	QQLQNPANTO	QQLQNPANTO	QQLQNPANTO	2671
2471	-----	QQLQNPANTO	QQLQNPANTO	QQLQNPANTO	2471
2556	-----	QQLQNPANTO	QQLQNPANTO	QQLQNPANTO	2556
2523	-----	QQLQNPANTO	QQLQNPANTO	QQLQNPANTO	2523
2703	-----	QQLQNPANTO	QQLQNPANTO	QQLQNPANTO	2703

FIG. 14

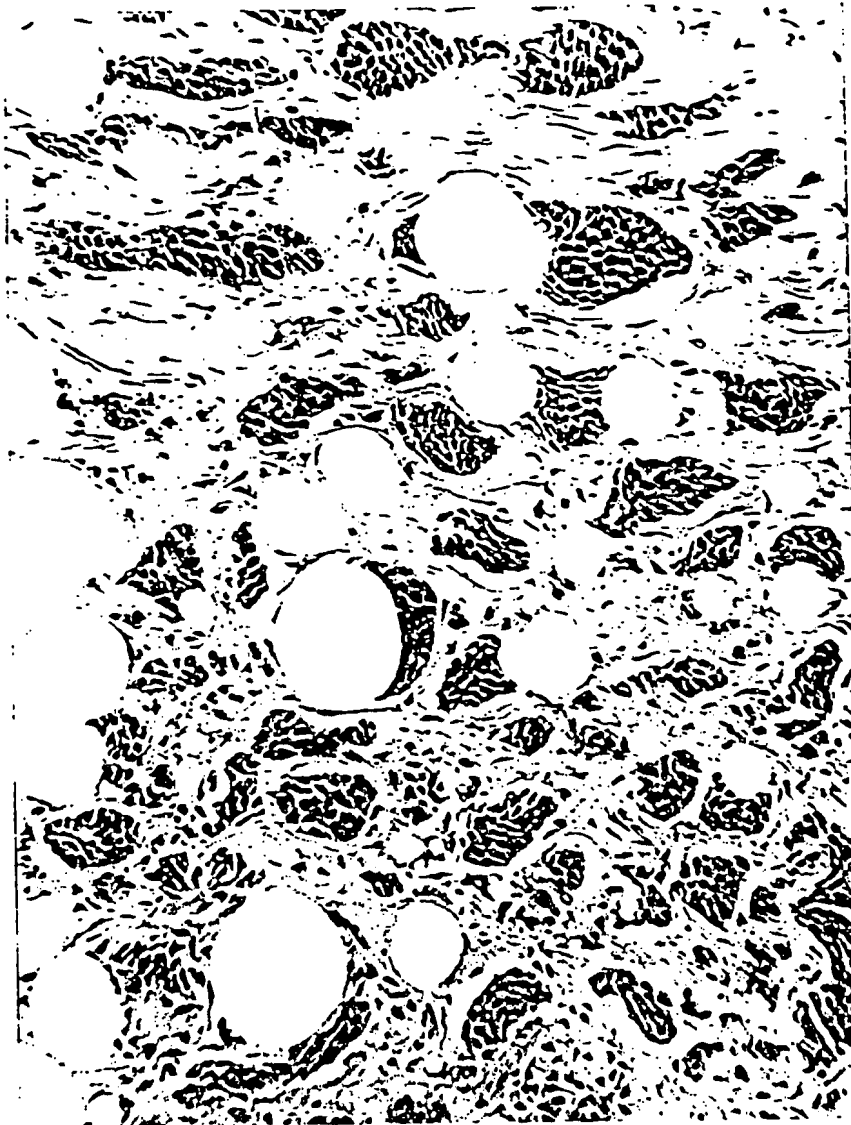


FIG. 15A

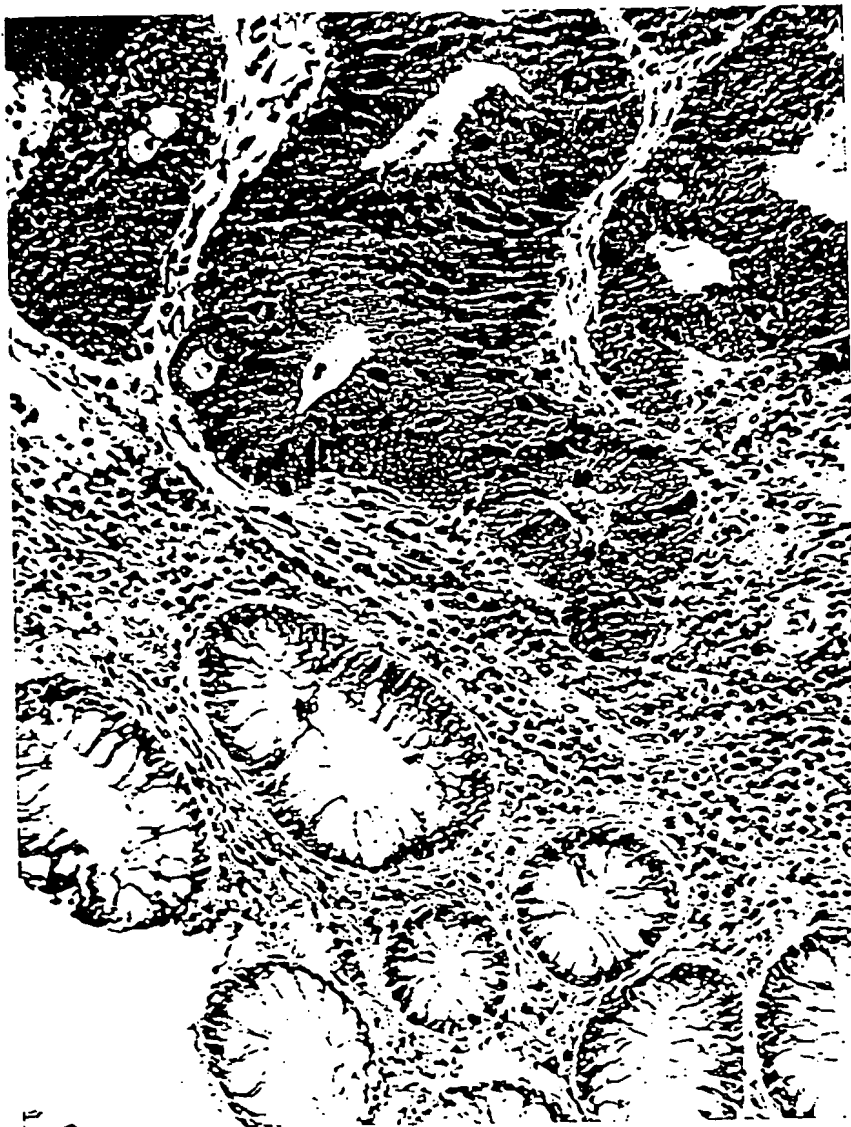


FIG. 15B



FIG. 16A



FIG. 16B





FIG. 17

10	20	30	40	50	60	70	80	90
GGAATTCGC	CCGCGCTCG	CCCGCTCTG	CTGTGGCGC	TGCTGGCGT	CTGGCTGTC	TGGCGGCGC	CCGCGCATG	ATTGCAGTG
P A L R P A L	L L W A L	L L A L L	L L A L L	L L A L L	L L A L L	L L A L L	L L A L L	L L A L L
100	110	120	130	140	150	160	170	180
CGAGATGGT	ATGAACCTG	TGTAATGAA	GGAATGTGT	TTACTATCA	CAATGGACA	GAATATGCA	AATGCCAGA	AGCTTCTTG
R D G Y E P C	V N E G M C	V T Y H N	G T G T G	G T G T G	G T G T G	G T G T G	G T G T G	G T G T G
190	200	210	220	230	240	250	260	270
GAGGAATAT	GTCAACATG	AGACCCCTG	GAGAAGACC	GCTGCCAGA	TGTTGGGACT	TGTTGGGCT	AGGCCATCT	GGGGAAGCC
G E Y C Q H R	D P C E K N	R C Q N G	G T G T G	G T G T G	G T G T G	G T G T G	G T G T G	G T G T G
280	290	300	310	320	330	340	350	360
AGGTGCGGT	GTGCTCAGG	GTTCACAGA	GAGGACTGC	AGTACTCA	ATCTCATCA	TGCTTTGCT	CTGACCTCT	CCTGAATGC
T C R C A S G	F T G E D C	Q Y S T S	H P C F V	S R P C L	N G >			
370	380	390	400	410	420	430	440	450
GACACATGC	ATATGCTCAG	CCGGATACC	TATGACTCA	CCTGTCAAGT	CGGTTTACA	GCTAAGGAGT	GCCAATGAC	GGATGCTGC
G T C H M L S	R D T Y E C	T C Q V G	F T G K E	C Q W T D	A C >			
460	470	480	490	500	510	520	530	540
CTGTCTCAT	CCTGTGCAA	TGGAGTACC	TGTACCACTG	TGGCAACCA	GTCTCTCTG	AAATGCTCA	CAGGCTTAC	AGGCAAGAA
L S H P C A N	G S T C T T	V A N Q F	S C K C L	T G F T G	Q K >			
550	560	570	580	590	600	610	620	630
TGTGAGACT	ATGTCAATGA	GTGTGACAT	CCAGGACAT	GCCAGATGG	TGGCACCTGC	CTCAACTGC	CTGGTCTTA	CCAGTCCAG
C E T D V N E	C D I P G H	C Q H G G	T G T G T	L N L P G	S Y Q C >			
640	650	660	670	680	690	700	710	720
TGCCCTCAGG	GCTTCACAGG	CCAGTACTGT	GACAGCTGT	ATGTGCCCTG	TGCACCTCA	CCTTGTCTCA	ATGAGGCAC	CTGTGGCAG
C P Q G F T G	Q Y C D S L	Y V P C A	P S P C V	N G G T C	R Q >			
730	740	750	760	770	780	790	800	810
ATGTGTGACT	TCACCTTTGA	GTGCACTGC	CTTCCAGTT	TTGAAGGAG	CACCTGTGAG	AGGAATATG	ATGACTGCC	TAACACAGG
T G D F T F E	C N C L P G	F E G S T	C E R N I	D D C P	N H R >			

## FIG. 17 CONT'D

820 \* TGTCAATG GAGGGTTTG TGTGGATGG GTCAACACTT ACAACTGCG CTTGCCCA CAATGACAG GACAGTTCTG CACAGAGAT  
 C Q N G G V C V D G V N T Y N C R C P P Q W T G Q F C T E D>  
 910 \* GTGATCAAT GCCTGCTGCA GCCCAATGCC TGTCAAAATG GGGGACCTG TGCACACCGC AATGAGGCT ATGGCTGTGT ATGTGTCAC  
 V D E C L L Q P N A C Q N G G T C A N R N G G Y G C V C V N>  
 1000 \* GGCTGGAGTG GAGATGACTG CAGTGAGAAC ATTGATGATT GTGCTTTCG CTTCTGTACT CCAGGCTCCA CCTGATCGA CCGTGTGGCC  
 G W S G D D C S E N I D D C A F A S C T P G S T C I D R V A>  
 1090 \* TCCTTCTCTT GCATGTGCC AGAGGGGAG GCAGGTCTCC TGTGTCATCT GGATGATGCA TGCATCAGCA ATCCTTGCCA CAAGGGGCA  
 S F S C M C P E G K A G L L C H L D D A C I S N P C E K G A>  
 1180 \* CTGTGTGACA CCAACCCCT AAATGGGCA TATATTGCA CCTGGCCACA AGGCTACAAA GGGGCTGACT CCACAGAAGA TGTGATGAA  
 L C D T N P L N G Q Y I C T C P Q G Y K G A D C T E D V D E>  
 1270 \* TGTGCCATGG CCAATAGCAA TCCTTGTGAG CATGCAGAA AATGTGTGAA CACGGATGGC GCCTTCCACT GTGAGTGTCT GAAGGTTAT  
 C A M A N S N P C E H A G K C V N T D G A F H C E C L K G Y>  
 1360 \* GCAGGACCTC GTTGTGAGAT GGACATCAAT GAGTGCATTT GAGTGCATTT CAGACCCCTG CCAGATGAT GCTACCTCTC TGGATAAGAT TGGAGCTTC  
 A G P R C E M D I N E C H S D P C Q N D A T C L D K I G G F>  
 1450 \* ACATGCTGT GCATGCCAGG TTTCAAAGT GTGCAITGTG AATTAGAAAT AATGAATGT CAGAGCAACC CTTGTGTGAA CAATGGCCAG  
 T C L C M P G F K G V H C E L E I N E C Q S N P C V N N G Q>  
 1540 \* TGTGTGATA AAGTCAATCG TTTCAGTGC CTGTGCTCTC TGGGCTTAC TGGCCAGTTG TGCAGATG APATTGAGA CTGTTCCAGT  
 C V D K V N R F Q C L C P P G F T G P V C Q I D I D D C S S>

## FIG. 17 CONT'D

1630	1640	1650	1660	1670	1680	1690	1700	1710
ACTCCGTGTC	TGAATGGGC	AAAGTGATC	GATCACCAG	ATGGCTATG	ATGCCAGTGT	GCCACAGGTT	TCACTGGTGT	GTGTGTGAG
T P C L N G A	K C I D H P	N G Y E C Q C	A T G F T G V	L C E>				
1720	1730	1740	1750	1760	1770	1780	1790	1800
GAGAACATG	ACAACGTGA	CCCGATCCT	TGCCACCAG	GTGAGTGCA	GGATGTATT	GATTCCTACA	CCTGCATCTG	CAATCCGGG
E N I D N C D	P D P C H H	G Q C Q D G I	D S Y T C I C	N P G>				
1810	1820	1830	1840	1850	1860	1870	1880	1890
TACATGGGG	CCATCTGCAG	TGACCAGATT	GATGAATGT	ACAGCAGCC	TGCGCTGAAC	GATGTCGCT	GCATTGACT	GGTCAATGGC
Y M G A I C S	D Q I D E C	Y S S P C L N	D G R C I D L	V N G>				
1900	1910	1920	1930	1940	1950	1960	1970	1980
TACCAGTGCA	ACTGCCAGCC	AGGCAGTCA	GGGTTAATT	GTGAATTA	TTTGTGAC	TGTCAAGTA	ACCTTGAT	CCATGGAATC
Y Q C N C Q P	G T S G V N	C E I N F D D	C A S N P C I	H G I>				
1990	2000	2010	2020	2030	2040	2050	2060	2070
TGTATGGATG	GCATTAATCG	CTACAGTGT	GTCTGCTAC	CAGGATTCAC	AGGCAGACA	TGTAACATTG	ACATTGATGA	GTGTGCTCC
C M D G I N R	Y S C V C S	P G F T G Q R	C I C P E G P	H P S C Y>				
2080	2090	2100	2110	2120	2130	2140	2150	2160
AATCCCTGTC	GCAAGGTGC	ACATGTATC	AACGGTGTA	ATGTTTCGG	CTGTATATGC	CCCGAGGAC	CCCATCACCC	CAGCTGCTAC
N P C R K G A	T C I N G V	N G F R C I C	P E G P H P S	C Y>				
2170	2180	2190	2200	2210	2220	2230	2240	2250
TCACAGGTGA	ACGAATGCT	GAGCAATCCC	TGCATCCATG	GAACTGTAC	TGGAGGTCTC	AGTGGATATA	AGTGTCTCTG	TGATGCAGGC
S Q V N E C L	S N P C I B	G N C T G G L	S G Y K C L C	D A G>				
2260	2270	2280	2290	2300	2310	2320	2330	2340
TGGGTGGCA	TCAACTGTGA	AGTGGACAAA	AATGAATGCC	TTTCGATCC	ATGCCAGAT	GGAGGAACCT	GTGACATCT	GGTCAATGGA
W V G I N C E	V D K N E C	L S N P C Q N	G G T C D N L	V N G>				
2350	2360	2370	2380	2390	2400	2410	2420	2430
TACAGGTGA	CTTCCAAGAA	GGGCTTTAAA	GGCTATTAAT	CCCAGGTGA	TATTGATGAA	TGTGCTCAA	ATCCATSCCT	GAACCAAGGA
Y R C T C K F	G F K G Y N	C Q V N I D E	C A S N P C L	N Q G>				
2440	2450	2460	2470	2480	2490	2500	2510	2520

* ACCTGCTTTG T C F	* ATGCATAAG D D I S	* TGCGTACACT G Y T	* TGCCACTGNG C H C	* TGCTGCCATA V L P Y	* CACAGGCAAG T G K	* AATTGTGAGA N C Q	* CAGTATTGGC T V L A	* TCCCCTGTTCC P C S>
2530 *	2540 *	2550 *	2560 *	2570 *	2580 *	2590 *	2600 *	2610 *
CCAAACCCTT P N P	GTGAGATGC C E N A	TGCTGTTTGC A V C	AAAGAGTCAC K E S	CANAATTTGA P N F E	GAGTTATACT S Y T	TGCTTGTGTG C L C	CTCCTGGCGT A P G M	GCAAGGTGAC Q G Q>
2620 *	2630 *	2640 *	2650 *	2660 *	2670 *	2680 *	2690 *	2700 *
R C T	I D I D	E C I	S K P	C M N H	G L C	H N T	Q G S Y	M C E>
2710 *	2720 *	2730 *	2740 *	2750 *	2760 *	2770 *	2780 *	2790 *
GTGTCACCAG C P P	GCITCAGTGG G F S G	TATGGACTGT M D C	E E D	I D D C	L A N	P C Q	N G G S	C M D>
2800 *	2810 *	2820 *	2830 *	2840 *	2850 *	2860 *	2870 *	2880 *
GGAGTAGTA G V N	T F S C	L C L	P G F	T G D K	C Q T	D M N	E C L S	E P C>
2890 *	2900 *	2910 *	2920 *	2930 *	2940 *	2950 *	2960 *	2970 *
AAGAATGGAG K N G	GGACCTGCTC G T C S	TGACTRACCTC D Y V	AACAGTTACA N S Y	CTTGCAAGTG T C K C	CCAGGACAGA Q A G	TTTGATGGAG F D G	TCCATTGTGA V H C	GAACAACATC N N I>
2980 *	2990 *	3000 *	3010 *	3020 *	3030 *	3040 *	3050 *	3060 *
AATAGATGCA N E C	CTGAGAGCTC T E S S,	CTGTTTCAAT C F N	GGTGGCAGAT G G T	GTGTTGATGG C V D G	GATTAACATCC I N S	TTCTCTTGCT F S C	TGTSCCCTGT L C P V	GGGTTTCAC G F T>
3070 *	3080 *	3090 *	3100 *	3110 *	3120 *	3130 *	3140 *	3150 *
GGATCCTTCT G S F	GCCTCCATGA C L H E	GATCAATGAA I N E	TGCAGCTCTC C S S	ATCCATGECCT H P C	GAATGAGGGA L N E	ACGTGTGTG T C V	ATGCGCTGGG D G L G	TACCTACCGC T Y R>
3160 *	3170 *	3180 *	3190 *	3200 *	3210 *	3220 *	3230 *	3240 *
TGCAGCTGCC C S C	CCCTGGGCTA P L G Y	CACCTGGGAAA T G K	AACTGTGAGA N C Q	COCTGGTGAA T L V N	TCTCTGCACT L C S	CGGCTCCCAT R S P	GTRAAAACAA C K N K	AGGTACTTGT G T C>
3250 *	3260 *	3270 *	3280 *	3290 *	3300 *	3310 *	3320 *	3330 *

## FIG. 17 CONT'D

ATTTCAGAAA AAGCAGAGTC CCAAGTGCCTA TGTCCATCTG CATGGCTGG TGGCTATTGT GAGTGCCCA ATGCTCTCTG TGACATAGCA  
 V Q K K A E S Q C L C P S G W A G A Y C D V P N V S C D I A>  
 3340 3350 3360 3370 3380 3390 3400 3410 3420  
 GCTCCAGGA GAGGTGTGCT TGTGACAC TTGTGCCAGC ACTCAGTGT CTGCAATCAAT GCTGGCAACA CGCATTTACTG TCAGTGCCCC  
 A S R R G V L V E H L C Q H S G V C I N A G N T H Y C Q C P>  
 3430 3440 3450 3460 3470 3480 3490 3500 3510  
 CTGGGCTATA CTGGGAGCTA CTGTGAGGAG CAACCTCGATG AGTGTGGTC CAACCCCTGC CAGCACGGG CAACATGCAG TGACTTCATT  
 L G Y T G S Y C E E Q L D E C A S N P C Q H G A T C S D F I>  
 3520 3530 3540 3550 3560 3570 3580 3590 3600  
 GGTGGATACA GATCGGAGTG TGTCCAGGC TATCAGGGTG TCAACTGGA GTATGAAGTG GATGAGTGC GATGAGTGC AGAATCAGOC CTGCCAGAT  
 G G Y R C E C V P G Y Q G V N C E Y E V D E C Q N Q P C Q N>  
 3610 3620 3630 3640 3650 3660 3670 3680 3690  
 GGAGGCACCT GTATTGACCT TGTGAACCAT TTCAAGTCT CTGCGCCACC AGGCACCTGG GGCCTACTCT GTGAAGAGAA CATGATGAC  
 G G T C I D L V N H F K C S C P G T R G L L C E N I D D>  
 3700 3710 3720 3730 3740 3750 3760 3770 3780  
 TGTGCCGGG GTCCCATTTG CCTTAATGCT GGTCAAGTCA TGAATAGAT TGGAGGCTAC AGTGTGCT GCTTGCCTG CTTTCTCTGG  
 C A R G P H C L N G G Q C M D R I G G Y S C R C L P G F A G>  
 3790 3800 3810 3820 3830 3840 3850 3860 3870  
 GAGCGTTCTG AGGAGACAT CAACGAGTGC CTCTCCACC COTGCACTC TGAGGCAGC CTGCACTGA TACAGCTCAC CAATGACTAC  
 E R C E G D I N E C L S N P C S S E G S L D C I Q L T N D Y>  
 3880 3890 3900 3910 3920 3930 3940 3950 3960  
 CTGTGTGTT GCGTAGTGC CTTTACTGG CCGCACTG CAACTTGTG CAATGTGT CCGCAGATGC CCTGCCTGAA TGAAGGACT  
 L C V C R S A F T G R H C E T F V D V C P Q M P C L N G G T>  
 3970 3980 3990 4000 4010 4020 4030 4040 4050  
 TGTGCTGTG CCACTAAT GCTGATGT TTAATTTGCC GTTGTCCCC GGAATTTCC GGGGCAAGT GCCAGAGCAG CTGTGGACAA  
 C A V A S N M P D G F I C R C P P G F S G A R C Q S S C G Q>  
 4060 4070 4080 4090 4100 4110 4120 4130 4140  
 GTGAATGTA GGAAGGGGA GCAATGTGTG CACACCGCT CTGACCCCG CTGCTTCTGC CCGAGTCCC GGAATGCGA GTCAGGCTGT

[illegible]

## FIG. 17 CONT'D

4960 \* CTCCTGGCCT CTCACGGCCAT ACAGGGGACC CTGTCATACC CTCCTGCTC TCTGCTCAGT GAATCCCTGA CTCAGAACG CACTACGCTC  
L L A S H A I Q G T L S Y P L V S V V S E S L T P E R T Q L>  
5050 \* CTCCTGCTCC TTGCTGTGCT TGTGTGATC ATTCTGTTA TTATCTGCT GGGGCTATC ATGCCAAAC GAAAGCTTA GCATGGCTCT  
L Y L L A V A V V I I L F I I L L G V I M A K R K R K H G S>  
5140 \* CTCCTGCTCC CTCAGGTTT CACTCTGCT CAGATGCA CGATGCA GCAATCACA GCTCTGCTG CCACTGGGAC AGGATGCTGT GGGGCTGAAA  
L W L P E G F T L R R D A S N H K R R E P V G Q D A V G L K>  
5230 \* AATCTCTCAG TGCAAGTCTC AGAAGCTAAC CTAATTGCTA CTGGAACAAG TGAACACTGG GTGATGATG AAGGCCCTCA GCCAAGAAA  
N L S V Q V S E A N L I G T G T S E H W V D D E G P Q P K K>  
5320 \* GTAAAGGCTG AAGATGAGG CTTACTCTCA GAAGAAGATG ACCCATTTA TCGACGGCCA TGGACACAGC AGCAGCTTGA AGCTGACAGC  
V K A E D E A L L S E E D D P I D R R P W T Q Q H L E A A D>  
5410 \* ATCCGTAGGA CACCATCGCT GGCTCTCACC CCTCTCTCAG CAGACAGGA GGTCGATGTG TTAGATGCA ATGTCCTGG CCCAGATGGC  
I R R T P S L A L T P P Q A E Q E V D V L D V N V R G P D G>  
5500 \* TGCACCCCAT TGATGTGCT TCTCTCCGA GGAGGCGCT CAGATTGAG TGATGAAGAT GAAGATGCA AGGACTCTTC TGCTAACATC  
C T P L M L A S L R G G S S D L S D E D E D A E D S S A N I>  
5590 \* ATCAGAGCT TGGTCTACCA GGGTCCAGC CTCAGGGCC AGACAGCCG GACTGTGAG ATGGCCCTGC ACCTTGCAGC CCGCTACTCA  
I T D L V Y Q G A S L Q A Q T D R T G E M A L H L A A R Y S>  
5680 \* CGGGCTGATG CTCGCCAAGG TCTCTGGAT GCAGTGCAG ATGCCAATGC CCAGACAAC ATGGGCGCT GTCCACTCCA TGCTGCTAGT  
R A D A A K R L L D A G A D A N A Q D N M G R C P L H A A V>

## FIG. 17 CONT'D

5770	5780	5790	5800	5810	5820	5830	5840	5850
GGAGCTGATG	CCCAAGGTGT	CTTCCAGATT	CTGATCGCA	ACCGAGTAAC	TGATCTAGAT	CCAGGATGA	ATGATGGTAC	TACACCCCTG
A A D A Q G V	F Q I L I R	N R V T D L D	A R M N D G T	T P L >				
5860	5870	5880	5890	5900	5910	5920	5930	5940
ATCCTGGCTG	CCCGCTGGC	TGTGAGGGA	ATGGTGGCAG	AAGTATCAA	CTGCCAACGG	GATGTGAATG	CAGTGGATGA	CCATGGAAAA
I L A A R L A	V E G M V A	E L I N C Q A	D V N A V D D	H G K >				
5950	5960	5970	5980	5990	6000	6010	6020	6030
TGTGCTCTTC	ACTGGGCAGC	TGCTGTCAAT	AATGTGAGG	CAACTCTTTT	GTTGTTGAAA	AATGGGCCCA	ACCGAGACAT	GCAGGACAC
S A L H W A A	A V N N V E A	T L L L L K N	G A N R D M Q	D N >				
6040	6050	6060	6070	6080	6090	6100	6110	6120
AAGGAAGAGA	CACCTCTGTT	TCCTGCTGCC	CGGAGGGGA	GCTATGAGC	AGCCAAGATC	CTGTAGACC	ATTITGCCAA	TCGAGACATC
F E E T P L F	L A A R E G S	Y E A A K I	L L D H F A	N R D I >				
6130	6140	6150	6160	6170	6180	6190	6200	6210
ADAGACATA	TGATCGTCT	TCCCGGGAT	GTTGGCTGGG	ATCGATGCA	CCATGACATT	GTCGGCCTTC	TGGATGAATA	CAATGTGACC
T D H M D R L	P R D V A R	D R M H D I	V R L L D E	Y N V T >				
6220	6230	6240	6250	6260	6270	6280	6290	6300
CQAAGCCCTC	CAGGCACCGT	GTTGACTTCT	GCTCTCTCAC	CTGTCACTG	TGGGCCCAAC	AGATCTTTCC	TCAGCCTGAA	GCACACCCCA
P S P P G T V	L T S A L S	P V I C G P N	R S F L S L	K H T P >				
6310	6320	6330	6340	6350	6360	6370	6380	6390
ATGGGCAAGA	AGTCTAGACG	CGGCACTGCC	AAGAGTACCA	TGCCTACTAG	CCTCCCTAAC	CTTGCCCAAGG	AGGCAAGGA	TGCCAAGGGT
M G K K S R R	P S A K S T	M P T S L P N	L A K E A K D	A K G >				
6400	6410	6420	6430	6440	6450	6460	6470	6480
ASTAGGAGGA	AGAAGTCTCT	CAGTGAAGAG	GTCCAACCTCT	CTGAGAGTTC	AGTAACCTTTA	TCCCTCTGTG	ATTCCCTAGA	ATCTCCTCAC
S R R K K S L	S L S E K V	Q L S E S S V	T L S P V D	S L E S P E >				
6490	6500	6510	6520	6530	6540	6550	6560	6570
ADGTATGTTT	CCGACACCAC	ATCCTCTCCA	ATGATTACAT	CCCCTGGAT	CTTACAGGCC	TCACCCAACC	CTATGTTGGC	CACCTGGCGCC
T Y V S D T T	S S P M I T	S P G I L Q A	S P N P M L A	T A A >				
6580	6590	6600	6610	6620	6630	6640	6650	6660



FIG. 17 CONT'D

CCCTGCTGCCC	CAGTCCTATGC	CCAGCATGCA	CTATCTTTTT	CTAACCCTCA	TGAAATGAG	CCTTTGGCAC	ATGGGGCCAG	CACGTGCTT	*
P P A	P V H A	Q H A	L S F	S N L H	E M Q	P L A	H G A S	T V L	*
6670	6680	6690	6700	6710	6720	6730	6740	6750	*
CCCTCAGTGA	GCCAGTGTCT	ATCCACACC	CACATTGTGT	CTCCAGGCAG	TGGCAGTGT	GGAAGCTTGA	GTAGGCTTCA	TCCAGTCCCA	*
P S V	S Q L L	S H H	H I V	S P G S	G S A	G S L	S R L H	P V P	*
6760	6770	6780	6790	6800	6810	6820	6830	6840	*
GTCPCAGCAG	ATTGATGAA	CCGATGCG	GTGATGAG	CCAGTACAA	TGACATGTT	GCTATGTCC	TGGCTCCAGC	TGAGGGCACC	*
V P A	D M N R	M E V	N E T	Q Y N	E M F	G M V	L A P A	E G T	*
6850	6860	6870	6880	6890	6900	6910	6920	6930	*
CATCTCTGGCA	TAGTCCCCA	GAGCAGGCCA	CCTGAAGGA	AGCACATAC	CACCCCTCG	GAGCCCTGC	CCCCCATGT	GACTTTCAG	*
H P G	I A P Q	S R P	P E G	K H I T	T F R	E P L	P P I V	T F Q	*
6940	6950	6960	6970	6980	6990	7000	7010	7020	*
CTCATCCCTA	AAGCAGTAT	TGCCCAACCA	GCGGGGGTCT	CCAGCCTCA	GTCCACCTGC	CCTCCAGTGC	TTCGGGGCC	CCTGCCACCC	*
L I P	K G S I	A Q P	A G A	P Q P Q	S T C	P P A	V A G P	L P T	*
7030	7040	7050	7060	7070	7080	7090	7100	7110	*
ATGTACCAGA	TTCAGAAAT	GGCCCGTTTG	CCCAGTGTGG	CTTCCCCAC	TGCCATGATG	CCCAGCAGG	ACGGGAGGT	AGCTCAGACC	*
M Y Q	I P E M	A R L	P S V	A F P T	A M M	P Q Q	D G Q V	A Q T	*
7120	7130	7140	7150	7160	7170	7180	7190	7200	*
ATTCTCCAG	CCTATCATCC	TTTCCAGCC	TCTGTGGCA	AGTACCCAC	ACCCCTTCA	CAGCACAGTT	ATGCTTCTC	AAATGCTGCT	*
I L P	A Y H P	F P A	S V G	K Y P T	P P S	Q H S	Y A S S	N A A	*
7210	7220	7230	7240	7250	7260	7270	7280	7290	*
GAGCGAACAC	CCAGTCACAG	TGCTCACTC	CAGGTGAGC	ATCCCTACT	GACACATCC	CCAGATCTC	CTGACCACTG	GTCAAGTTCA	*
E R T	P S H S	G B L	Q G E	H P Y L	T P S	P E S	P D Q W	S S S	*
7300	7310	7320	7330	7340	7350	7360	7370	7380	*
TGACCCCACT	CTGCTTCTGA	CTGCTCATAT	GAGACACCA	GCCTTACCC	TGGGGTGTCT	GGAGGAGTCT	ACCGGGGACC	TGGGACACAC	*
S P B	S A S D	W S D	V T T	S P T P	G G A	G G G	Q R G P	G T H	*
7390	7400	7410	7420	7430	7440	7450	7460	7470	*

## FIG. 17 CONT'D

ATGCTCAGC CACCACACAA CAACATGCAAG GTTATATCGT CAGACAGTCC ACCTCCAGTG TAGACACATA ACTGACTTTT GTAATATGCTG  
 M S E P P H N N M Q V Y A  
 7480 \* 7490 \* 7500 \* 7510 \* 7520 \* 7530 \* 7540 \* 7550 \* 7560 \*  
 CTGAGGACAA AATGAAGGTC ATCCGGGAGA GAAATGAAGA AATCTCTGGA GCCAGCTTCT AGAGGTAGGA AAGAGAAGAT GTTCTTATTC  
 7570 \* 7580 \* 7590 \* 7600 \* 7610 \* 7620 \* 7630 \* 7640 \* 7650 \*  
 AGATAATGCA AGAGAGCAAA TTCTGTCAGTT TCACCTGGTA TCTGCAAGGC TTATTCATTA TTCTAATCTA ATAAGACAAG TTGTGCGAAA  
 7660 \* 7670 \* 7680 \* 7690 \* 7700 \* 7710 \* 7720 \* 7730 \* 7740 \*  
 TGCAAGATGA ATACAGCCCT TGGGTCCATG TTTACTCTCT TCTATTTGGA GAATAAGATG GATGCTTATTT GAAGCCCGAGA CATTCCTTGCA  
 7750 \* 7760 \* 7770 \* 7780 \* 7790 \* 7800 \* 7810 \* 7820 \* 7830 \*  
 CCTTGGACTG CATTTTAAGC CCTGCAGGCT TCCTGCCATAT CCATGAGAG ATTCTACACT AGCTGCTCTGT TGGGAATTTAT GCCCTGGAAT  
 7840 \* 7850 \* 7860 \* 7870 \* 7880 \* 7890 \* 7900 \* 7910 \* 7920 \*  
 TCTGCCCTGAA TTGACCTACG CATCTCCTCC TCCCTTGGACA TTCTTTTGTG TCATTTGGT GCTTTTGGTT TTGCACCTCT CGGTGATTGT  
 7930 \* 7940 \* 7950 \* 7960 \* 7970 \* 7980 \* 7990 \* 8000 \* 8010 \*  
 AGCCCTACCA GCATGTATATA GGGCAAGACC TTGTGCTTTT TGATCANTCT GGGCCCATGAA AGCAACTTTC GTCTCCTTTC CCTCTCTGTC  
 8020 \* 8030 \* 8040 \* 8050 \* 8060 \* 8070 \* 8080 \* 8090 \* 8100 \*  
 TTCCCGGTAT CCTTGGAGT CTCACAAGGT TTACTTTGGT ATGGTTCTCA GCACAAACCT TTCAAGTATG TTGTTTCTTT GGAAAAATGGA  
 8110 \* 8120 \* 8130 \* 8140 \* 8150 \* 8160 \* 8170 \* 8180 \* 8190 \*  
 CATACTGTAT TGTGTTCTCC TGCAATATC ATTCTCGGAG AGAGAAGGG AGAAGATAC TTCTCTCAA CAAATTTTGG GGCAGGAGA  
 8200 \* 8210 \* 8220 \* 8230 \* 8240 \* 8250 \* 8260 \* 8270 \* 8280 \*  
 TCCCTTCAAG AGGCTGCACC TTAATTTTTC TTGCTGTGT GCAGGTCTTC ATATAAACTT TACCAGGAAG AAGGTGTGA GTTTGTGTTT  
 8290 \* 8300 \* 8310 \* 8320 \* 8330 \* 8340 \* 8350 \* 8360 \* 8370 \*  
 TTTCTGTGTA TGGGCCCTGGT CAGTGTAAAG TTTTATCCTT GATAGTCTAG TTACTATGAC CCTCCCACT TTTTAAAC CAGAAAAAGG  
 8380 \* 8390 \* 8400 \* 8410 \* 8420 \* 8430 \* 8440 \* 8450 \* 8460 \*  
 TTTGGAATGT TGGAAATGACC AAGAGACAAG TTAATCTGTG CAAGAGCCAG TTACCCACCC ACAGTCCCC CTACTCTCTG CCAAGCAATC

## FIG. 17 CONT'D

8470	8480	8490	8500	8510	8520	8530	8540	8550
CATTGACTGC	CTGRTATGGAA	CACATTGTGC	CCAGATCTGA	GCAITCTAGG	CCCTGTTTAC	TCACTCACCC	AGCATATGAA	ACTAGCTCTTA
8560	8570	8580	8590	8600	8610	8620	8630	8640
ACTGTTGAGC	CTTTCCCTTTC	ATATCCACAG	AAGACACTGT	CTCAAAAGTT	GTACCCCTGC	CAITTAGGAC	TGACCTTTCC	TTAGCCCAAG
8650	8660	8670	8680	8690	8700	8710	8720	8730
GGACCCAGTG	ACAGTTGTCT	TCGGTTTGC	AGATGATCAG	TCTCTACTGA	TTATCTTGCT	GCITTAAGGC	CTGCTCACCA	ATCTTTCTTT
8740	8750	8760	8770	8780	8790	8800	8810	8820
CACACCGTGT	GGTCCGNGTT	ACTGGTATAC	CCAGTATGTT	CTCACTGAAG	ACATGGACTT	TATATGTTCA	AGTGCAGGAA	TTGGAAGAATT
8830	8840	8850	8860	8870	8880	8890	8900	8910
GGACTTGTTT	TCTATGATCC	AAAACAGCCC	TATAAGAAGG	TTGGAAGAAG	AGGAACCTATA	TAGCAGCCCT	TGCTATTITC	TGCTACCAAT
8920	8930	8940	8950	8960	8970	8980	8990	9000
TCITTTTCTC	TGAAGCGGCC	ATGACATTCC	CTTTGGCAAC	TAACGTAGAA	ACTCAACAGA	ACATTTTCTT	TTCCPAGAGT	CACCTTTTAG
9010	9020	9030	9040	9050	9060	9070	9080	9090
ATGATAATGG	ACAACTATAG	ACTTGTCTAT	TGTTCAAGCT	GATTCGCCCT	CACCTGAATC	CACCTCTGT	ATTCATGCTC	TTGGCAATTT
9100	9110	9120	9130	9140	9150	9160	9170	9180
CTTTTGACTTT	CTTTTAAAGG	CAGAGCAATT	TTAGTTAATT	GTAGATAAAG	AATAGTTTTC	TTCCCTCTTT	CCTTGGGCCA	GTTAATAATT
9190	9200	9210	9220	9230	9240	9250	9260	9270
GGTCCATGGC	TACACTGCAA	CTTCCGTTCA	GTGCTGTGAT	GCCCATGACA	CCTGCAAAAT	AAGTTCTGCC	TGGGCATTTT	GTAGATATTA
9280	9290	9300	9310	9320	9330	9340	9350	9360
ACAGGTGAAT	TCCCGACTCT	TTTGGTTTGA	ATGACAGTTC	TCAATTCCTC	TATGGCTGCA	AGTATGCAATC	AGTGCCTTCCC	ACTTACCTGA
9370	9380	9390	9400	9410	9420	9430	9440	9450
TTTGTCTGTC	GGTGGCCCCA	TATGGAACCC	CTGGGTGCT	GTTGGCATAA	TAGTTTACAA	ATGGTTTTTT	CAGTCTTATC	CAAAATTTAT
9460	9470	9480	9490	9500	9510	9520	9530	9540

FIG. 17 CONT'D

GAACCAACAA AATATATTAC TTCTGCCCTG AGATAAGCAG ATTAAGTTTG TTCAATCTCT GCATTATCT CTCCATGCG CAACATTCG  
 9550 \* 9560 \* 9570 \* 9580 \* 9590 \* 9600 \* 9610 \* 9620 \* 9630 \*  
 TCAGCCTCTT TCATAGTG TGCAACATTT ATCATTTCTAA ATGGTGAATC TCTGCCCTTG GACCCATTTA TTATTCACAG ATGGGAGAA  
 9640 \* 9650 \* 9660 \* 9670 \* 9680 \* 9690 \* 9700 \* 9710 \* 9720 \*  
 CCTATCTGCA TGGACCTCA CCATCTCTG TGCAGCACAC ACAGTGCAG GAGCCAGTG CGATGGCGAT GACTTCTTC CCTTGGGAAT

TCC